



☐ 1: Transgenic Res 2002 Aug;11(4):425-35



Related Articles, Links

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Tayt Varsian								

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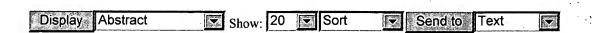
The use of the uromodulin promoter to target production of recombinant proteins into urine of transgenic animals.

Zbikowska HM, Soukhareva N, Behnam R, Chang R, Drews R, Lubon H, Hammond D, Soukharev S.

Plasma Derivative Department, Holland Laboratory, American Red Cross, MD 20855, Rockville, USA.

A uromodulin promoter has been isolated, sequenced, and used to generate two sets of transgenic mice for expression of the lacZ marker gene and for production of the human recombinant erythropoietin (rhEPO) in urine. We demonstrated that the 5.6kb fragment of the uromodulin gene containing the 3.7-kb promoter area and, both the first exon and part of the second exon, were sufficient to provide kidneyspecific expression of the lacZ gene. Histological analysis of the lacZ expression pattern revealed beta-galactosidase activity specifically in the thick limb of Henle's loop. However, due to random integration of the transgene, ectopic expression was detected in some transgenic lines. Analysis of the EPO-transgenic mice showed that rhEPO was secreted into the urine of founder mice (up to 6 ng/ml). We were able to breed and analyze only two sublines with a very low expression level of rhEPO (up to 260 pg/ml). All of our transgenic mice expressing rhEPO in urine developed disease symptoms similar to polycythemia in humans. These included a considerable increase in red blood cell counts, hemoglobin concentration, and hematocrit concomitant with severe thrombocytopenia, all of which were detected in the rhEPO-expressing mice. Although our model did not prove to be beneficial for commercial production of rhEPO, we concluded that the uromodulin promoter could be useful for expression of other important therapeutic proteins into the urine of transgenic animals.

PMID: 12212844 [PubMed - in process]



Write to the Help Desk NCBI | NLM | NIH Department of Health & Human Services Freedom of Information Act | Disclaimer

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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1: /cgn2_6/ptodata/2/

2: /cgn2_6/ptodata/2/

3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-232-463-14
US-09-641-38-161
US-09-36107A-8
US-08-356-107A-8
US-09-323-195A-3
US-08-628-417-6
US-08-97-289-11
US-08-92-334-1
US-08-92-334-1
US-08-92-334-2
US-08-92-334-2
US-08-92-334-3
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US-09-424-283-5
US-09-331-195A-6
US-09-377-648-4
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3-14/c 4 Application US/08: 5670367 5670367 NPORMATION: NT: DORNER, F. NT: DORNER, F. NT: SCHEIFLINGER, F. NT: FALKNER, F. OF SCHENCES: 52 CONDENCE ADDRESS: SSEE: FOLEY & Lardn. T: 1800 Diagonal Ro. Alexandria NA TYPE: Floppy disk PIER: IBM PC compati. TING SYSTEM: PC-DOS, NRE: Patentin Relea APPLICATION UMBER: US/0 NG DATE: CATION NUMBER: US/0 NG DATE: CATION NUMBER: EP 9 NG DATE: CATION NUMBER: EP 9 NG DATE: 26-AUG-1991 TOR POR SEQ ID NO: 1 DHONE: (703)83-4109 TOR POR SEQ ID NO: 1 DE CHARACTERISTICS: INUCLEIC acid UDEDNESS: single OGY: PTZPPT-F1s TE SURCE: TE SURCES: THE 7218 base pairs THE SOURCE: THE SURCES: THE TZPPT-F1S	960 2223 2447 255 731 1733 1733 1447 1700 1700 1700 1700 1700 1700 1700
US/0823: EER, F. ECGMBINJ 52 Lardner al Road mpatible mpatible TA: US/08/M Release TFION: TFION: 1991 TFION: 29,76 EP 91 -1991 -1991 -1991 -1091	<b>41241344442344443</b>
US/08232463  GER, F. F. G. RECOMBINANT FOWLPOX VIRUS 52 S: Lardner nal Road, Suite 500  mal Road, Suite 500  mal Road, Suite 500  mal Road, Suite 500  sep 91 114 300.6 G-1991 ATION: n A: US/08/232,463 EP 91 114 300.6 GG-1991 MOER: 30472/114 IMMU ORMATION: 6-9300 4109  NO: 14: US/08/232/114 IMMU ORMATION: 6-9300 4109  NO: 14: US/08/232/114 IMMU ORMATION: 6-9300 4109	US-09-071-035-25 US-08-257-073-4 US-09-014-969-14 US-09-257-583-5 US-08-251-405A-2 US-09-073-569-1 US-08-913-014A-18 US-09-276-599-14 US-09-276-599-14 US-09-2443-041A-27 US-08-897-340-4 US-09-252-329-4 US-09-251-645-11 US-09-328-111-177 US-09-370-838-151 US-09-370-838-151 US-09-370-838-151 US-08-931-999-4
-	Sequence 25, Appli Sequence 4, Appli Sequence 14, Appli Sequence 5, Appli Sequence 1, Appli Sequence 18, Appli Sequence 11, Appli Sequence 17, Appli Sequence 27, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 177, App Sequence 11, Appli Sequence 177, App Sequence 177, App Sequence 151, Appli Sequence 151, Appli Sequence 151, Appli Sequence 177, App Sequence 151, Appli

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Matches 13; Conservative '
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US-09-641-638-161/c
; Sequence 161, Application US/09641638
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1304
NUMBER OF ESQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 161
LENGTH: 1001
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
CURRENT FILING DATE: 2000-02-13
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: US/09/502,330
PRIOR FILING DATE: 199-05-07
PRIOR FILING DATE: 199-05-07
PRIOR APPLICATION NUMBER: US/09/275,267
PRIOR APPLICATION NUMBER: US/09/275,267
PRIOR APPLICATION NUMBER: US/09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
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APPLICANT: Blumenf
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                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM TILLE REFERENCE: GENSET.051CP1
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NAME/KEY: misc_binding
NAME/KEY: 481.500
LOCATION: 481.500
OTHER INFORMATION: 12-747-302.mis1, potential
OTHER INFORMATION: 12-747-302.mis2, potential complement
LOCATION: 502.521
OTHER INFORMATION: 12-747-302.mis2, potential complement
LOCATION: 200.219
OTHER INFORMATION: upstream amplification primer
OTHER INFORMATION: upstream amplification primer
                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                     OTHER INFORMATION: 12-747-302 : polymorphic base C
                                                                                                                                    NAME/KEY: allele
LOCATION: 501
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NAME/KEY: primer_bind
LOCATION: 646..666
COTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_binding
LOCATION: 489..513
COTHER INFORMATION: 12-747-302 potential probe
US-09-641-638-161
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US-08-936-107A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08936107A Patent No. 6403306 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                    NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REGISTRATION NUMBER: 77-9
REFERENCE/DOCKET NUMBER: 77-9
REFERENCE/DOCKET NUMBER: 303) 499-8080
TELECOMMUNICATION INFORMATION: 303) 499-8080
TELECOMMUNICATION INFORMATION: 303 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stephens, APPLICANT: Swartley,
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: PatentIN DATA: //o.//opering
                                                            TELEFAX: (303) 495-8089
TELEFAX: (303) 495-8089
INFORMATION FOR SEQ ID NO: ESCOURAGE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 5064 base pairs
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Col
                                                                                                                                                                                                                           PILING DATE: 23-bi-
FILING DATE: 536
CLASSIFICATION: 536
PRIOR APPLICATION DATA: US 08/827,622
APPLICATION NUMBER: US 08/827,622
APPLICATION 09-APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 80303
                                                                                                                                                                                                  FILING DATE: 09-APR-1997
FILING DATE: 09-APR-1997
AFTORNEY/AGENT INFORMATION:
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TOPOLOGY: no
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Similarity 50.8%;
99; Conservative
                                 STRANDEDNESS:
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                                                  nucleic acid
                       not relevant
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23-SEP-1997
       DNA (genomic)
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                                         double
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pred. No. 0.014;
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HYPOTHETICAL: FEATURE:

NAME/KEY: LOCATION: US-08-936-107A-8

FEATURE: NAME/KEY: FEATURE:

LOCATION:

NAME/KEY: NAME/KEY: LOCATION:

Query Match Best Local S

Matches 122;

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## us-09-605-042a-37.rni

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RESULT 4
US-09-323-195A-5
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APPLICANT: Pullman,
APPLICANT: Cairney,
APPLICANT: Perrera,
APPLICANT: Perrera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1537 CCCTTACGGGATAGGTAATGCCTCAAAAATCATTGTAGAAACTTTATTAAAGAATAGATA 1596
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09323195A patent No. 6462257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1597 ABATGTTATACTTAATAACAGAAAATGGCGTAAACTTAAAAGAGACCCTAGCGCTTTCT 1656
                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/323,195A
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 19 90-06-01
CURRENT FILING DATE: 19 90-06-01
SEQ ID NOS: 19
SEQ ID NOS: 19
SEQ ID NOS: 19
LENGTH: 565
LENGTH: 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1657 TTCGAGATAGTAAATTTAACTTTTTAAGATATTTTTCTGCTAAAAATTTGCAAAGAATT 1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 CACCAACCAGAAATGACATTCACCACCTAGGATTGAGAAAAAAGAATATTAGGAACTTTTA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 ACGGGCAAAGGATACAAACAGTTCAGAAAAGAATAAATAGTAAGCAAATGAAAAGATAAC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Perrera, Ranjan TITLE OF INVENTION: METHODS TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1777 CAACCTTAAAAGAAAAT 1793
                                                                    OTHER INFORMATION: n at 489 is OTHER INFORMATION: n at 503 is OTHER INFORMATION: n at 522 is OTHER INFORMATION: n at 522 is OTHER INFORMATION: n at 533 is OTHER INFORMATION: n at 543 is OTHER INFORMATION: n at 543 is OTHER INFORMATION: n at 543 is OTHER INFORMATION: n at 544 is OTHER INFORMATION: n at 564 is OTHER INFORMATION: n at 564 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 CAAAGATGAAAGTTAAT 332
Ouery Match 184.52 Best Local Similarity 84.52 Best Local Similarity 84.52 Generative Matches
                                                                                                                                                                                                           TYPE: DNA ORGANISM: Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCTTTTTCATCAAAGAACCGCAAAAGTAAATAATGATAAGATGTTTCTCACTTTTCCA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.5%;
h 47.5%;
Similarity 47.5%;
22; Conservative
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479..1597
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1599..3236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3309..4052
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4054..4917
                                                                                                                                                                                                                                                                                                                                                     VICILIN-LIKE SEED STORAGE PROTEIN GENE PROMOTER AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                   Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 4; Length 5064; Pred. No. 0.049;
                                 2.5%;
                     Score 40.2; DB 4; Length 565;
Pred. No. 0.024;
O; Mismatches 8; Indels
                                                                                                   000000000
                                                                                                        222222
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                                                       Gaps
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US-09-323-195A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Calrney,
APPLICANT: PETTERS,
APPLICANT: PETTERS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA; pinus taeda; ORGANISM: pinus taeda
US-09-323-195A-3
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CURRENT APPLICATION NUMBER: 05/09/323,195A
CURRENT FILING DATE: 1999-06-01
CURRENT FILING NOS: 1990
NUMBER OF SEQ ID NOS: 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANI: CAIINEY, JOHN
APPLICANI: CAIINEY, JOHN
APPLICANI: PETTERA, RADJAN, VICTINI-LIKE SEED STORAGE PROTEIN GENE PROMOTER AND TITLE OF INVENTION: METHODS OF USING THE SAME TITLE OF INVENTION: METHODS OF USING THE SAME TITLE OF INVENTION: METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-08-628-417-6
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Query Match
Best Local Similarity 100.0%;
Best Local Similarity 100.0%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08628417
Patent NO. 5627054
Patent INFORMATION:
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GILLESPIE, DAVID OR PRIMER ASYMMETRIC TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC TITLE OF INVENTION: POLYMERASE CHAIN REACTION TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3, 646.
                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION: 435
ATOGRNEY AGENT INFORMATION: 539,908
NAME: BIFFONI, ULYSSES J
REGISTRATION UUMBER: 39,908
REGISTRATION UNBER: DAM
REFERENCE/DOCKET NUMBER: DAM
REFERENCE/DOCKET NUMBER: DAM
REFERENCE/DOCKET NUMBER: 11.58
TELEPHONE: 410-571-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAAAG 40
1 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAAAG 40
1 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAAAG 40
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FLOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: // // 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO 3
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL ADDRESSEE: DEFENSE COMMAND COUNSEL (AMSCB-GC) STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC) CITY: ABERDEEN PROVING GROUND STATE: MARYLAND
                                                                                         TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09323195A
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                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pullman, Gerald
                                                                             LENGTH: 240 bases
TYPE: nucleic acid
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pred. NO. 0.02;
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                                                                                                                                                                                                    DAM 398-94
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## us-09-605-042a-37.rni

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MOLECULE TYPE: N
HYPOTHETICAL: N
ANTI-SENSE: YES
US-08-628-417-6
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CURRENT SPLICATION NUMBER: US/09/323,195A
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 199-06-01
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
SEO ID NO 1
IENGTH: 341
TYPE: DNA
ORGANISM: Pinus taeda
ORGANISM: Pinus taeda
US-09-323-195A-1
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Query Match
Best Local Similarity 50.3%;
Best Local Similarity 50.3%;
Matches 97; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pullman, John
APPLICANT: Cairney, John
APPLICANT: Perrera, Ranjan
APPLICANT: Perrera, VICILIN-LIKE SEED STORAGE PROTEIN GENE PROMOTER AND
TITLE OF INVENTION: METHODS OF USING THE SAME
TITLE OF INVENTION: METHODS OF USING 195A
TITLE OF INVENTION: METHODS OF USING 195A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 GAAAAAAAAAAAAAACATTCTTATGGGGGGATAAACGGGCAAAGGATACAAACAGTTCAGAAAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                             US-08-978-289-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%;
Query Match
Best Local Similarity 100.0%;
Best Local Similarity 100.0%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 GAATAAATAGTAAGCAAATGAAAAGATAACTTCCTTTTTCATCAAAGAACCGCAAAAGTA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 AATAATGATAAGA 298
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                                                                PATENT NO. 6361939

PATENT NO. 6361939

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

Caux, Christophe

APPLICANT:

Lebecque, Serge J.E.

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION:

TITLE OF 
                                                                                                                                                                                                                                                                                                                                                                                                          1, Application US/09323195A
5. 6462257
  CORRESPONDENCE ADDRESS:
ADDRESSEE DNAX Research Institute
                                       NUMBER OF SEQUENCES:
ADDRESSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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0.041;
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PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

MAPPLICATION UNMBER:

FILING DATE: 11-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION UNMBER: US 60/031,806

APPLICATION UNMBER: 27-NOV-1996

FILING DATE: 17-NOV-1996

FILING DATE: 11PCPAMATION:

ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: misc_feature NAME/KEY: misc_feature LOCATION: 49.51 LOCATION: /note-original formation: /note-original formation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650)496-1204
TELEFAX: (650)496-1204
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 901 CAL
CITY: Palo Alto
STATE: Californ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ching, Edwin P. 4,090
REGISTRATION NUMBER: DX
REFERENCE/DOCKET NUMBER: DX
REFERENCE/DOCKET NUMBER: DX
REFERENCE/DOCKET NUMBER: DX
REFERENCE/DOCKET NUMBER: DX
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Best Local Sin
Matches 108;
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FILING DATE: 25-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3172 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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IOCATION: 481
OTHER INFORMATION: /note= "may be T"
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                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                               113 AAAAAGAATATTAGGAACTITTATTTTCTTGAAGTTATAGCAAAGAAAGGAAAAAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 994
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 994
                                                                                                                                                                                                                    2882 GGAATATGGATATGAAGTGCAGAAGCAAGCAAGTTACCACAAGATGGGGGCTATCACTCAA 2823
                                                                                                                                                                                                                                                                      173 AAAAACATTCTTATGGGGATAAACGGGCAAAGGATACAAACAGTTCAGAAAAGAATAAA 232
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2762 TTTATTTGATGCCTTCATCTTTACAGCCCAGCTAAGCAATCCC 2720
                                                                                                                                                             233 TAGTAAGCAAATGAAAAGATAACTTCCTTTTTCATCAAAGAACCGCAAAAGTAAATAATG 292
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                                                                                                               GAAAGAACAGTTGGTTAGCGAAGTTTCTCTATTATCAAAAAAATTTAAAAAATACTTTGAG
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Pred. NO. 0.15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                    1209
                                                                                                                                                                                                                                                                                         1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                         1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FALKNER, F. TITLE OF INVENTION: RE
                                                                                                                                                                                                                                                                                                                                                                                                                     942 CTTGATTCACAGAGCATCTGGTCCAATGATGTCTGAATTATCTGCTGTCTCTGACCTTCA 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                     GCACCCCTTTTCTCCTGGAGCAGCCTGGCTTCAGATTCTGGCCTCTGCTTGGCTCCACTT 1181
                                                                                                                                       AGGATGGCATTTGCTTTGGAATTAAGTGGCCACAAGTACACATCCTGGTGGGGACGATGA 1121
                                                                                                                                                                                                                    31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DORNER, F.
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US-08-992-334-1
                                                                                                                                                                                                                                            US-08-992-334-1
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Patent No. 591967
                                                                                                                                    Matches
                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (626) 577-88 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/992,334 FILING DATE: 17-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1242 TAACTAAAGAACCTCTTGTTGCCAAAAGGTATAAAACAGAGCCCTTGTAGCTGT 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: [626] 795-9900
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                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
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APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                       AGTGTGGATATAGAGCAAGTTATGCAAAGGTTCTTGATGCTGAAACGGGGGAAATAAAAT 2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THALL STATES THAT TAKE TAKE THE TAKE THAT TAKE TAKE TAKE THE TAKE 
                                                                                                                                    123;
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EDNESS: both
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350 West Colorado Boulevard, Suite 500
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                                                                                                                                Conservative
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                                                                                                                                Score 38.4; DB 2;
Pred. No. 0.25;
0; Mismatches 141;
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                                                                                                                                           141;
                                                                                                                                                                                                  Length 3792;
                                                                                                                                           Indels
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US-08-302-752-1
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Patent No. 6025190
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                           FILING DATE: 12-MAR-1993
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 3792 base pairs
LENGTH: 3792 base pairs
TERNTE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2827 TTTATTGAGAGGAGTGATTATTGAATAAATAAAGCCCCCTGACGAAGTCGAAGGGGGT 2886
                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
US-08-302-752-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: THEI
NUMBER OF SEQUENCES: 3
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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COMPOTER: IBM PC compatible
COMPOTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: PATENTION DATA:
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Matches 123; Conserv
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                                                                                                                                                                 164 GGGAAAAAAAAAAAAAACATTCTTATGGGGGATAAACGGGCAAAGGATACAAACAGTTCAGAA 223
                                                                                                                  224 AAGAATAATAGTAAGCAAATGAAAAGATAACTTCCTTTTTCATCAAAGAACCGCAAAAG 283
                                                                 284 TARATRATGATAAGATGTTTCTCACTTTTCCACAAAGATGAAAGTTAATGCCCAGGGTGG 343
2887
                       344
                                            TTTATTGAGAGGAGGATTATTGAATAAATAAAAGCCCCCTGACGAAAGTCGAAGGGGGT 2886
                      CTGAGTACTGTGCTGGGATTGTGA 367
TTTTATTTTGGTTTGATGTTGCGA 2910
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milarity 46.6%;
Conservative
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Pred. No. 0.25;
0; Mismatches 141; Indels
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RESULT 12
US-08-992-334-2
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                                                                                                                                                                                                                                    TOPOLOGY: Circular NOLECULE TYPE: DNA (genomic) US-08-992-334-2
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Query Match
Best Local Similarity 46.6%;
Hest Local Similarity
Matches 123; Conservative
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PRIOR APPLICATION NUMBER: US 08/302,752
RIPLICATION NUMBER: 1994
RIPLICATION 24-DEC-1994
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                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: FR FR92/03034
APPLICATION NUMBER: FR FR92/03034
APPLICATION NUMBER: 13-MAR-1992
APPLICATION DATE: 13-MAR-1992
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CS
TELECOMMUNICATION INFORMATION:
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FILING DATE: 24-DEC
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Prout, D. Bru
REGISTRATION NUMBER:
                                                                                                                                         4089 AGTGTGGATATAGAGCAAGTTATGCAAAGGTTCTTGATGCTGAAACGGGGGAAATAAAAT 4148
                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                  PELEPHONE:
                                               4209 CTTADADGGGTATTGAAAGATACAGAGAATGGAAGTTGAATTAAGTACAACAATAGA 4268
                                                                                                                  164 GGGAAAAAAAAAAAAACATTCTTATGGGGGATAAACGGGCAAAGGATACAAAACAGTTCAGAA 223
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4269 TTTATTGAGAGGAGGATTATTGAATAAATAAAAGCCCCCCTGACGAAAGTCGAAGGGGGT 4328
                                                                                                                                                                                                                                                                                                      ENGTH
                                                                    224 AAGAATAAATAGTAAGCAAATGAAAAGATAACTTCCTTTTTCATCAAAGAACCGCAAAAG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08992334
                      284 TARATARTGATRAGATGTTTCTCACTTTTCCACAAAGATGAAAGTTAATGCCCAGGGTGG 343
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350 West Colorado Boulevard, Suite 500
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                                                                                                                                                                                                                                                                                                        5234 base pairs
                                                                                                                                                                                                                                                                                                                                       (626)
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(626) 577-8800
626) 577-8800
SEO ID NO: 2:
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12-MAR-1993
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4329 TTTTATTTTGGTTTGATGTTGCGA 4352

344 CTGAGTACTGTGCTGGGATTGTGA 367

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TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-302-752-2
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                                                                                                Sequence 3, Application US/08992334
Patent No. 5919678
GENERAL INFORMATION:
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Best Local Similarity
Matches 123; Conserv
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INFORMATION FOR SEQ ID NO: 2
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APPLICATION NUMBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR/93/0
APPLICATION NUMBER: WO FR/93/0
APPLICANT: Gruss, Alexandra
APPLICANT: Maguin, Emmanuelle
TITLE OF INVENTION: PLASMID
NUMBER OF SEQUENCES: 3
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LENGTH: 5234 base pair
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TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                            TTTTATTTTGGTTTGATGTTGCGA 4352
                                                                                                                                                                                                                                                             CTGAGTACTGTGCTGGGATTGTGA 367
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Patent No.

Sequence 3, Application Patent No. 6025190 GENERAL INFORMATION:
APPLICANT:

us/08302752

TITLE OF INVENTION: NUMBER OF SEQUENCES:

THERMOSENSIBLE PLASMID

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US-08-992-334-3
RESULT 15
US-08-302-752-3
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Best Local Similarity
Matches 123; Conserv
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PRIOR APPLICATION DATA:
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NAME: Prout, D. Bruce
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REGISTRATION NUMBER: 20
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FR FR92/03034 FILING DATE: 13-MAR-1992
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TOPOLOGY: ci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Christie Parker & Hale, LLP STREET: 350 West Colorado Boulevard, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/302,752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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CLASSIFICATION: 435
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PRIOR APPLICATION UNMEER: FR 9203034
APPLICATION NUMBER: JAMAR-1992
FILING DATE: JAMAR-1992
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Search completed: February 17, 2003, 16:14:37 Job time : 121.862 secs
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Best Local Similarity 99.5%;
Matches 1449; Conservative
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                                                                                                                                                                                                                    CCTCAAAGAGGCAATGCTGTGGATCACTGTCATATTTCCTGCTCAGCCTGAGTTCACATG 577
                                                                                           GCTGAACCAAGCCCTGTCATTCTCTGCCCCATGACTGCGCATCACCAAAACAGCATCGGC
                                                                                                                         0;
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pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                         kidney-specific gene; urine-producing cell; urine; transgenic animal; antibody; heterodimeric fertility fibrinogen; enzyme; uromodulin gene promoter; ss.
                                                                               partial DNA sequence of the bovine uromodulin gene promoter.
                                                                                          25-JUL-2000
                                                                                                                                                                                                                                                                                                               ATGAGCACCCCTTTTCTCCTGGAGCAGCCTGGCTTCAGATTCTGGCCTCTGCTTGGCCTCC 1177
                                                                                                                                                                                                                                                                     WO200015772-A2
                                                Bos sp
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                 16-SEP-1999;
                                                                                                                                                                                                                            TCTGGTTTCAGGAAGG 1494
                                                                                                                                                TCTGGTTTCAGGTAAG 1553
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                   99WO-IB01609
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid construct containing kidney-specific promoter, useful recombinant production of protein, e.g. antibody, in the urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 626 BP; 184 A; 147 C; 130 G; 165 T; 0 other;
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                                                                                                                                CCCATTAAAATAATTAAGAAACAGAACCAGAGGATCATTGGAGGAGAGATTGCCAGTGGG
                                                                                                                                                                                                                               GGCACAGCTGTGACCCCCATGTCAATCATTTGGGGTCTCTACCTATTAGGGAAAAGAACA 1356
                                                                                                                                                                                                                                                                   CACTTTGTGCTTTTCAATGACCAAGAAAATCCCAGGCCCTTGGAATTGTTTACTCAGTTA
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                                                                 GGACAGATGTATATATATAGATATGAAAGTCACCTACTTGTAAAAGGATTAATTCTACCT 1536
                                                                                                                                                          ACAACCACCTCACAGCCTAGAAAAGGAAAACACTGTGTCAAAAGGGAAAAATATTCCACC
                                                                                                                                                                        ACAACCACCTCACAGCCTAGAAAAGGAAAACACTGTGTCAAAAGGGAAAAATATTCCACC 1416
                                                                                                        GGCACAACTGTGACCCCAGTGTCAATCATTTGGGGGTCTCTACCTATTAGGGAAAAGAACA
                           TTCTGGTTTCAGGTAAGGCTATCTGCAG 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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llarity 94.1%;
Conservative
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Pred. No. 4.3e-142;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 620 BP; 164 A; 155 C; 138 G; 163 T; 0 other;
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                                                                                                                                                                                                                                                      CATTTGCTTTGGAATTAAGTGGCC---ACAAGTACACATCCTGGTGGGGACGATGAGCAC
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                                                                                              ACTTTGTGCTTTTCAATGACCAAGAA-AATCCCAGGCCCTTGGAATTGTTTACTCAGTTA
                                                                                                                                                                                                  GTGTTTCAGAAGGGTGCCCTCTCCAAGACAGGTGCACCTCCCATCTGGGGCAGTGAATAT 173
TCAGCTCCTCTTGCTTGTGTCTGGATTCTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  containing kidney-specific of protein, e.g. antibody,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 266.2;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                             ---AGGCTGATCTCATGAGAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uromodulin; promoter; kidney; urine; heterologous gene; treatment;
therapy; gene expression; pharmaceutical; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse uromodulin promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                         exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTGGGGCAAATGTGTATATATATATGAGGCACA----TCATCACCAGACTAACTCT
                                                                                           WO200029608-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTTTCTGGCTTCAGGTAAGGCTATCTGTAGC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTTTCTGGTTTCAGGTAAGGCTATCTGCAGC 1565
                               12-NOV-1999;
                                                              25-MAY-2000.
   13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       /label= Exon 1
/cons_splice= (
7115..7892
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8273..8274
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8074..8818
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bel Intron 1
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                                                                                               AAA12450 standard;
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As New methods to produce heterologous recombinant proteins in urine CC require the use of a DNA molecule which is a kidney-specific require the use of a DNA molecule which is a perably linked to a CC promoter, such as the uromodulin promoter, operably linked to a CC uromodulin promoter expresses the heterologous gene encoding a biologically active protein the CC uromodulin promoter expresses the heterologous gene in vivo in the CC urine. The recombinant proteins produced may be useful for treating CC urine. The major advantages of using this urine-based system CC over milk-based systems are the ability to harvest the product soon CC of the stand throughout the life of the animal irrespective of sex CC over milk-based systems are the ability to harvest the product constitution from CC urine. In addition, livestock urine is a proven, currently utilised CC source of pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New kidney-specific promoter useful for production animals as urinary bioreactors, is operably linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 7a-7h; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9345 BP; 2622 A; 2072 C; 2084 G; 2565 T; 2 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1163 CCTCTGCTTGGCTCCACTTTGTGCTTTTCAATGAGCAAGAAAA-TCCCAGGCCCTTGGAA 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6737 CTTGGGCTTAGGTCTACCTTGTCCTTGCCCAGGTCCAAGAAAAGGCCCAGAACCTTGGCA 6796
                                                                                                                                                                                                                                                                                                                                                                                                                                            6797
                                                                                                                                                                                                                                                                                                                                                                      1282 GCCCTTGTAGCTGTGGGCACAGCTGTGACCCCCATGTCAATCATTTGGGGTCT-CTACCT 1340
                                                                                                                                                                                                                                                                                                                                                  6856 GACCTTGTATTTCCAGGCACAGGTGTGACCCCAATGTCAATCATTTTGTGTGTCTAACTCCC
                                                                                                                                                                                                                                           1401 GGAAAAATATTCCACCCCCATTAAAATAATTAAGAAACAGAACCAGAGGATCATTGGAGG 1460
                                                                                                                                          7036
                                                                                                                                                                         1461 AGAGATTGCCAGTGGGGGACAGATGTATATATATAGATATGAAAGTCACCTACTTGTAAA 1520
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                                                                      7096
7152
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                                 1581 CCACTTCTCCCATCT 1595
                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTTTTGCCAGTTAATGTCTAACTGAGGAATGTCTTGCTGCCAAAAAGGT-GAAAACAGA 6855
                                                                                                                                                                                                                                                                                  AGGGGAAAAACTAACAACAACAGACTCATGGCTTGGAAAAGGTGAATTCTATGCCAAAAG 6975
                                                                                                                                                                                                                                                                                                                   ATTAGGGAAAAGAACAACCACCTCACAGCCTAGAAAAGGAAAACACTGTGTCAAAAG 1400
                                                                                                                                                                                                              AGGATTAATTCTACCTTTCTGGTTTCAGGTAAGGCTATCTGCAGCTCTCACTTCTCCCTAG 1580
                                                                                                                                          8.8%;
Similarity 65.7%;
86; Conservative
   CCACTTCTCCTCTAT
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pred. No. 1.8e-28;
0; Mismatches 142;
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to a heterologous
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25-JUL-2000

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid construct containing kidney-specific promoter, useful recombinant production of protein, e.g. antibody, in the urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kidney-specific gene; urine-producing cell; urine;
transgenic animal; antibody; heterodimeric fertility hormone; collagen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3; 48pp; English
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                                                                                                                                                                                                                                                                                                                        1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 625 BP; 168
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 1505
                                                                1448
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                                                                                                                                                                                                                             328
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        TICTGGCCTCTGCTTGGCTCCACTTTGTGCTTTTCAATGACCAAG-AAAATCCCAGGCCC 1215
                                                                                                                                                                                        CTACCTATTAGGG----AAAAGAACAACAACCACCTCACAGCCTAGAAAAGGAAAACACTG 1391
                                                                                                                                                                                                                                                                                                             TIGGAATIGITACICAGTIAATITCIAACIAAAGAACCICTIGIIGCCAAAAGGGIATAA 1275
                                                                                                                                                                                                                                                                                                                                                      TCCTGCCCCTTTGGTATTTCCACCTTGTCCTTGCCCAGGTCCAAGAAAAAAGCCCCAGAACC 268
 GTCACCTACTTGTAAAAGGATTAATTCTACCTTTCTGGTTTCAGGTAAGGCTATCTGCAG
                                                                TGCCAAATGGGAAGAAAATTCTGACCCCCACAGAAACAATCTCAAGAGGCAGAAGCAGA 507
                                                                                                                 TGTCAAAAGGG----AAAAATATTCCACCCCCATTAAAATAATTAAGAAACAGAACCAGA 1447
                                                                                                                                                               CTAACTACCAGAGGAAAAACTAACAACAACAGCCTCATGGTTTGGAAAAGGTGAACTCTA 447
                                                                                                                                                                                                                             AACAGAGACCTTGTATTTCCAGGCACAGGTGTGACCCCCAATGTCAATCATTTTCTGTCT
                                                                                                                                                                                                                                          AACAGAGCCCTTGTAGCTGTGGGCACAGCTGTGACCCCC-ATGTCAATCATTTGGGGTCT 1334
                                                                                                                                                                                                                                                                                          TTGGCACTGCTTTGCCAGTTAATGTCTAACCGAGGAATGTCTTGCTGCCAAAAGGT-GCA
                                 294;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 141.4; DB 2
Pred. No. 2.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                         111; Indels
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ARESULT 6
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AA180 AA180 XX
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                                                                                                                                                                                                          Matches 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI89272 standard; cDNA; 419
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diagnosing and treating e.g. leukaemia, i
disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200164835-A2
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                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 9332; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001; 2001WO-US04927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                                                                     Sequence 419
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                                227
                                                                                                                                                                                                                                     Local Similarity
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AAAAAAAAAAAACATTCTTATGGGGGATAAACGGGCAAAGGATACAAACAGTTCAGAAAAG
                                                                                      1565
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                                                                                                                                                                                                       Conservative
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2000US-0577409.
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                                                                                                                                                                                                                                                                                                                     BP; 202 A; 69 C; 47 G; 62 T; 39
                                                                                                                                                                                                                                  3.1%;
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                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                     Score 50.6; DB 22; Pred. No. 0.0013;
                                                                                                                                                                                                             Mismatches 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for preventing
                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or; haematopoiesis;
leukaemia;
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RESULT 7
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ID ABL32032 standard; DNA; 9770
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                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcrartive bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                 Claim 1; SEQ ID NO 5; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                        Sequence 9770 BP; 2479 A; 109 C; 2325 G; 4857 T; 0 other
                                                                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                        WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                   Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2001; 2001WO-EP07537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                               (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399 AANANAAATAAAAA 414
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                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAACATCGCTGAAAA 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTACTGTGCTGGGATTGTGAACTAACTGTTATAGATCTCTCTGGGGTGCTGTTTGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune system associated
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                                                                                                                                                                                                                                                methylation
                                                                                                                                                                                                                                                                                                                                 Piepenbrock C,
  Conservative
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              2.9%;
                                                                                                                                                                                                                                                                                                                                   Berlin
 0;
              Score 47.6; DB Pred. No. 0.036;
 Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene SEQ ID NO:
                            DB 24;
 Indels
                            Length
                             9770;
 0;
Gaps
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77 ACCAACCAGAAATGACATTCACCACCTAGGATTGAGAAAAAAGAATATTAGGAACTTTTAT 136

Query Match

Sequence 411 BP; 214 A; 24 C; 64 G; 107 T; 2 other;

Score 47.2;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine; pent's
                                                                                               cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynuclectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammanomodulatory activity and activity, tissue growth factor activity, hammanomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                              Tang
                         at ftp.wipo.int/pub/published_pct_sequences
                                         Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 8655; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                         Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation, vaccine; peptide therapy; stem cell growth factor; haemato tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polynucleotide SEQ ID NO 8655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3878
                                                                                     treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system disorders; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001
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                                                                                                                                                                                                     encoded
                                                                                                                                                                                                                   invention relates to human polynucleotides (AAI79941-AAI93841) and
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                                                                                                                                                                                                                                                                                                                                                                               Liu C,
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RESULT 9
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Matches 9
                                                                                                       of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFDI and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with diagnosis or therapy of diseases associated with congenital heart disease, related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or the amplification of the 350 sequences, (II) and/or their complementary sequences, (II) and/or their complementary and as oligomer problems for detecting the discount of the 350 sequences, (II) and/or their complements and as oligomer problems for detecting the discount of the 350 sequences, (II) and/or their complements and the supplication of the 350 sequences, (II) and/or their complements and the supplication of the 350 sequences, (II) and/or their complements and the supplication of the 350 sequences or the supplication of the supplication supplies the supplication supplies the supplication supplies the supplies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid (1) comprising a sequence a least 18 bases in length of a segment of chemically pretreated DNA least 18 bases in length of a segment of chemically pretreated DNA least 18 bases in length of a segment of chemically pretreated DNA least 18 bases associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes listed of genes associated with development selected from 87 genes as general genes as general genes as general genes as general general genes as general g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes assisted and the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a segment of chemically pretreated by the sequence of a sequence of a
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01-SEP-2000;
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                                                                    as oligomer probes for detecting the cytosine methylation state and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATGAAAAGATAACTTCCTTTTTCATCAAAGAACCGCAAAAGTAAATAATG
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94; Conservative
             nucleotide polymorphisms (SNPs).
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                                                                                                                                                                                                                                                                                 gene;
                                                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                           Human immune
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                                          Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                    30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17183 BP; 5157 A; 149 C; 3266 G; 8611 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     As The invention relates to identifying metastatic tumour cells comprising CC testing them for hybridisation to at least one cDNA sequence CC testing them for hybridisation to at least one cDNA sequences.

CC testing them for hybridisation to at least one cDNA sequences for metastatic CC testing the complete gene, functional fragments, CC testing the cDNA sequences are markers for metastatic CC potential in breast and pancreatic tumours, useful for diagnosis, for contributing potential agents for treatment of cancer, e.g. antibodies. CC particularly for staging cancers and selection of therapy antibodies. CC identifying potential agents for treatment of cancer, e.g. antibodies. CC against proteins encoded by the cDNA sequences or antisense sequences. CC against proteins encoded by the cDNA sequences allowing its cc functional analysis, including study of metastasis-specific regulatory concerns analysis, including study of metastasis-specific regulatory concerns analysis, including study of metastasis of cc sequences for clarification of molecular regulatory mechanisms of cc metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                   Identifying metastatic tumor cells and screening for antitumor comprises hybridization to specific cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 TAGGTTTGGGGGAAAGGGGTTTTCTTCCCTTTTTTGTTTTTGGAAAAGAAAAAGVAAAGAAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 GGGGAAAAAAAAAAACATTCTTATGGGGGATAAACGGGCAAAGGATACAAACAGTTCAGA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 AAAGAATAAATAGTAAGCAAATGAAAAGATAACTTCCTTTTTCATCAAAGAACCGCAAAA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ67061 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 GTAAATAATGATA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; anglogenesis; methylation; eye disease; glaucoma; tumour; finflammation; rheumatoid arthritis; disebetic retinopathy; antiulcerds; inflammation; theumatoid inflammatory bowel disease; crohn's disease; macular degeneration; inflammatory bowel disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antitheumatic; antiarthric; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human angiogenesis associated polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ67061;
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                 The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) bases of chemically pretreated DNA of angiogenesis-associated genes (II) bases of chemically pretreated DNA of angiogenesis-associated genes (II) also bases of chemically pretreated to the methylation status and/or having sequences (ABO66971-ABO67178) or their complements. (I), also bases of the methylation status and related to evaluate the methylation status and treatment of eye diseases, proliferative retinopathy, single-nucleotide polymorphisms, in angiogenesis related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, macular degeneration caused by neovascularisation, diabetic retinopathy, macular degeneration bowel diseases, ulcers and diabetic retinopathy, macular degeneration caused by neovascularisation of the composition of the compo
                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid fragments from chemically treated angiogenesis associated genes, useful for determining methylation angiogenesis associated genes treatment of cancer status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                далалалалала 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 schacht 0;
                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 91; 41pp + Sequence Listing; German.
             The sequence data
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; pred. No. 0.014;
; pred. No. 0.014;
1; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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Query Match
Best Local
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                                                                                                                                                                                                                                                  14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL11189 standard;
       The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and polypeptides are also useful for isolating compounds with cytostatic polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                                                                                                     Human breast cancer expressed polynucleotide 3646.
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                         Claim 1;
                                                                                                                                                                          Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252
polypeptides activity.
                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                          15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ecification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                              peptide useful
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2000US-0189167.
2000US-0192099.
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2000US-0205230.
2000US-0211315.
2000US-0220534.
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                                                                                                                                                                                                                                                                                                                                                                                                cancer;
                                                                                                          671; 3695pp; English.
                                                                                                                                                                          Y, Wang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA;
                                                                                                                                as a marker for the diagnosis of breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                 cell marker; cytostatic; ss
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                                                                                                                                                                          Steinmann
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ID ABQ15588 standard;
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Best Local S
Matches 89
This invention describes a novel method for determining the degree of cc methylation of a particular cytosine in a motif 5'-CpG-3', present in a cc genomic sample of DNA. The sample is treated chemically to convert cc cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one cc member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers cc and the degree of hybridisation to both classes is determined from the CC and the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method CC classes of oligomers, the degree of methylation is calculated. The method CC is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory constrains etc., particularly by detecting mutations or single nucleotide contrains of calculated of the contrains (SNP's); and (ii) for differentiation of cell or tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide
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                                                                                                                                                                                                                                                                        Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA \,
                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gastrointestinal; respiratory system;
SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                  Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                             05-SEP-2000;
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                                                                                                                                                                                                                                             Claim 12;
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les 89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock
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2000DE-1044543
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51.7%;
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                                                                 Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
This invention describes a novel method for determining the degree methylation of a particular cytosine in a motif 5'-CpG-3', present
                                      Claim 12; 56pp + Sequence Listing;
                                                                                                                                                   Olek A,
                                                                                                                                                                                                       01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                01-SEP-2001; 2001WO-EP10074.
                                                                                                                                                                                                                                                                          07-MAR-2002.
                                                                                                                                                                                                                                                                                                    WO200218632-A2
                                                                                                                                                                                                                                                                                                                                                        drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide for detecting cytosine methylation SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ15589 standard; DNA; 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                             (EPIG-)
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125;
                                                                                                                                                                                                                                                                                                                                                                                        cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                             EPIGENOMICS
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Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracii, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of ollgonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the rapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously; ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                       ACAAAGATGAAAGTTAA 331
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Search completed: February Job time: 373.012 secs 17, 2003, 09:19:52

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Copyright (c) 1993 - 2003 Compugen Ltd.
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AL09998 Drosophil
AL109339 Drosophil
AL109339 PřESTOBAB
BQ451939 PřESTOBAB
BQ451939 Drosophil
AL074609 Drosophil
AL266197 Tetraodon
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Submitted (02-UN-1999) Genoscope - Centre National de Sequencage

Part of a Submitted (02-UN-1999) Genoscope - Centre National de Sequencage

Part of a Submitted (02-UN-1999) Genoscope - Centre National : seqref@genoscope.cns fr

Part of a Submitted (02-UN-1998) Genoscope - Centre National : sequence was carried out as part of a part of the Sequence was carried out as part of a sequence was part of the Drosophila collaboration with the Berkeley Drosophila melanogaster genome using these BACs. For further in Bogp Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and please see http://www.fruitfly.org the Bogp Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and please see http://www.fruitfly.org the Bogp Drosophila and melanogaster BAC library was prepared by Kazutoyo Oscogawa and please see http://www.fruitfly.org the Bogp Drosophila and melanogaster BAC library was prepared by Kazutoyo Oscogawa and please see http://www.fruitfly.org the Bogp Drosophila and melanogaster BAC library was prepared by Kazutoyo Oscogawa and please see http://www.fruitfly.org the Bogp Drosophila and please see http://www.fruitfly.org the Bogp Drosophila and melanogaster BAC library was prepared by Kazutoyo Oscogawa and please see http://www.fruitfly.org the Bogp Drosophila and please see http://www.fruitfly.org the Bogp Droso
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Eukaryota; Endoptera; Diptera; Brachycera; Muscomorpha;
Neoptera; Endoptera; Drosophila.
Ephydroidea; Drosophilade; Drosophila.
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Determination of this BAC-end sequence was carried out as parcollaboration with the European Drosophila Genome Project (El http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was ma
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2; Mismatches 10
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Brachycera; Muscomorpha;

Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Loses 1 to 903)

Genoscope. Direct Submission

AL074609.1 GI:4953985

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span 191006 EVRY cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr

By 191 91006 EVRY cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr)

Web: www.genoscope.cns.fr)

By 191 www.genoscope.cns.fr)

By 191 www.genoscope.cns.fr)

Collaboration with the European Drosophila Genome Project (EDGP) -

Collaboration with the European Drosophila melanogaster BAC

Collaboration with the European Billaud at CEPH (Centre

Collaboration with funding provided by a MRC

http://www.edgp.ebi.ac.uk - This Drosophila melanogaster

Collaboration with funding provided by a MRC

http://www.edgp.ebi.ac.uk - This Drosophila melanogaster

The DNA was prepared from embryos by Alain Bucheton

Library (Dros BAC) by Man was prepared from embryos by Alain Bucheton

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Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D.,

Marra, W., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B.,

Marra, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I.,

Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Carr, L., Grow, A.,

Bewers, Y., Gibbons, M., Ritter, E., Bennett, J., Carr, L., Grow, A.,

Tasgareishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A.,

Maguire, J., Wilson, R. and Sibley, D.

Wasterston, R., Wilson, R. and Sibley, D.

Wasterston, R., Wilson, R. and Sibley, D.

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Wasterston, R., and R., and
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plasmodium falciparum plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; plasmodium.
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Library was constructed by Debopam Chakrabarti DNA Library was constructed by Debopam Chakrabarti For Library was noiversity Genome Sequencing a Sibley washington University obtaining a Clone please contact: L. David Sibley obtaining a Clone please contact: L. David Sibley obtaining a Clone please Contact: L. David Sibley observants. Agup from Gibco. Seq primer: 40UP from Gibco. Seq primer: 10Cation/Qualifiers
                                                                         3.2%;
                                            Score 52.6; DB 14;
pred. No. 0.045;
                                     red. No. 0.045;
Mismatches 134;
                                                                Length 413;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                          GSS; genome survey sequence.

Tetraodon nigroviridis.

Tetraodon nigroviridis

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;

Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
                                                                                  Bernot, A., Fizames, C., Williams, and Weissenbach, J.
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2 (bases 1
                                                                               Tetraodon nigroviridis DNA
                                                                                                                                                       Roest-Crollius, H., Jaillon, O., Das:
Bernot, A., Fizames, C., Wincker, P.,
                                                                                                                                                                                                                                       Tetraodontidae;
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/db_xref-"taxon:7227"
/clone-"BACR36I18"
/clone_lib-"RPCI-98"
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006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                             to 1045)
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Pred. No. 0.05
35; Mismatches
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84 AGAAATGACATTCACCACCTAGGATTGAGAAAAGAATATTAGGAACTTTTATTTTCTTC
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                                                                                                                                                                                                                                                                                             Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Belontin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Liore Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, C., Ozier-Kalogeropoulos, C., Casaregola, A., Casaregola, A., Casaregola, C., Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kluyveromyces lactis.
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Kluyveromyces lactis
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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clone BAOAB030C03 of library BAOAB
Kluyveromyces lactis, genomic surve
AL429183
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Direct Submission
Submitted (12-APR-2000)
Submitted (12-APR-2000)
This sequence is a single read and was generated as Scale clone-end sequencing project of the Tetraodon scale clone-end sequencing please take a look at
                                                                                                                                                                                                                                    Saurin, W., Tekaia, F., Toffano-Nioche, C., Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome. For more information, please t
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 1065)
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/db_xref="taxon:99883"
/clone="068003"
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/note="Genoscope
155 c 166
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to 1065)
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqrefgenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, 2990saccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansennii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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Drosophila melanogaster genome survey sequence T7 end of B
BACN01C10 of DrosBAC library from Drosophila melanogaster
fly), genomic survey sequence.
                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                     Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail : - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                            Drosophila melanogaster.
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Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brool
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi.P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legas,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McClos
                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3040)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens, clone IMAGE:5210832, BC025769
                                                                                                                                                                                                           Gaithersburg, Maryland; web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                   Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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/note="end : T7"
288 c 267 g
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/db_xref="taxon:7227"
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                                          Legaspi, R.,
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                                                                                                              Brooks, S.,
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Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

Touchman, J.W.,

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RESULT 10
BE420576
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Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.

International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                      Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERMANY
Fax: 49 30 171683
                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare.
Hordeum vulgare
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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This clone was selected for full length sequencing because it
                                                                                                  Contact: Herrmann RG
                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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Email: herrmann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
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This clone
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669 c 669 g 743 t
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/db_xref="taxon:9606"
/clone="IMAGE:5210832"
/tissue_type="Blood, adult leukocytes"
/clone_11b="NIH_MGC_118"
/lab_host="DH10B"
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53.1%;
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                                                                                                                                                                                                      Unpublished (2002)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ398892
544 bp mRNA linear EST 22-MAY-2002
NISC_mol2b07.x1 Soares NXEG Xenopus laevis cDNA clone IMAGE:5278813
                                                             Plate: LLAM11704 row: D c
Seg primer: -21M13 forward
                                                                                                           Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                      Cancer Insitute, Xenopus
                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                  African clawed
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                                                                                              into@image.ll
                                                                                                                                                                                                                                                                                                  (bases 1 to 544)
                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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/organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="14 day old"
/note="Vector: pBluescriptSK(-);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xreff"taxon:4513"
/clone="hww000.001"
/clone_lib="ITEC HMM Barley Leaf Library"
/tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare"
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Pred. No.
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                                                                               column:
                                                               primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104;
                                                                                                                                                                                                                                                                                                             Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R
Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wrg,
G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H.
                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SP_0155_B1_E05_SP6E Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=155 Col=9 Row-J, DNA sequence.
                                                                                                                                                        California Institute of Technology Pasadena California 91125, USA
                                                                                                                                                                                                                                           Proc. Natl. Acad. Sc
                                                                                                                      Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                       Contact: Cameron, RA, Davidson, EH, Division of Biology 156-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus purpuratus.
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                                                                                                                                                                                                                                                                                                 Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotidae; Strongylocentrotus
                                                Seq primer: SP6
Class: BAC ends
                                                                                    Email: acameron@caltech.edu
Plate: 155 row: J column:
                                                                                                                                                                                                                                                                             sea urchin genome project: Sequence scan, virtual map,
                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 877)
quality sequence stop: 877.
Location/Qualifiers
1. .877
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8 c 17 g 134 t
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Best Local
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                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTATAGCAAAGAAAGGGGAAAAAAAAAAAACATTCTTATGGGGGATAAACGGGCAAAGGAT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
AL287681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis genome
105D21 of library G from Tetra
                                                         This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                     2 (bases 1 to 629)
Roest-Crollius, H., Jaille
Bouneau, L., Billault, A.,
                                                                                                                                                                                                                                                                                                                               Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetie: Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                                                                                                      Charaterization and repeat analysis of the confreshwater pufferfish Tetraodon nigroviridis
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Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
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                                                                                                                          Submitted (12-APR-2000)
                                                                                                                                           Direct Submission
                                                                                                                                                          Genoscope.
                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                     Weissenbach, J.
                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodontidae; Tetraodon.
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/clone_lib="Strongylocentrotus purpuratus,
urchin, sperm genomic BAC library"
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/db_xref="taxon:7668"
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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|t,A., Quetier,F., Saurin,W.,
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enome survey sequence PUC-Ori end
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Euteleostei; Neoteleostei;
rpha; Tetraodontiformes;
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                                                                                                                                                                                                                      compact genome of the
                                                                                                                                                                                                                                                                       Fizames, C.,
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone BAOAB031B08 of library BAOAB from strain CLIB Kluyveromyces lactis, genomic survey sequence. AL429343 AL429343.1 GI:12212537
             Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY Cedex, FRANCE. (E-mail: sequencingenoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var uvarum, Saccharomyces
                                                                                                                                                                                                                            Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M. Genomic exploration of the hemiascomycetous yeasts: 11. Kluyveromyces lactis
                                                                                                                                                                                                                                                                                                                                                                                                    Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
                                                                                                                      Direct Submission
                                                                                                                                     Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; 1 (bases 1 to 867)
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                                                                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 487 (1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.
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/note="Genoscope sequence ID : COBG105CB11SP1-end
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                                                                                                                                                                                                                 Unpublished (2000)
Contact: Herrmann RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
                                                                                                                                                Menzinger Str. 67, D-80638 Munchen GERMANY Fax: 49 30 171683
                                                                                                                                                                                                                                                         Expressed Sequence Tags
                                                                                                                                                                                                                                                           International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
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                                                                                  International Triticeae EST Cooperative (ITEC) http://wheat.pw.usda.gov/genome.
                                                                                                                                 Email: herrmann@botanik.biologie.uni~muenchen.de
                                                                                                                                                                                           Botanisches Institut der LMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE420736.1 GI:9418579
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                                            1. .1309
/organism="Hordeum vulgare'
/cultivar="Barke"
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/clone_lib="BA0AB"
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/strain="CLIB 210"
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Search completed: February 17, 2003, 16:07:13 Job time : 2104.74 secs
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/dev_stage="14 day old"
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/note="Vector: pBluescriptSK(-);
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	RESULT 1  S75961  LOCUS THPO-Tamm. Horsfall protein (promoter) [cattle, Genomic, 626 nt].  DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM Bos taurus Bovinae; Bos Bos taurus Bovinae; Bos Title Bovine and rodent tamm-horsfall protein (THP) genes: cloning,	ALIGNMENTS	27 48.6 3.0 235685 3 26095310 26087242 298877 Caenorhabdi 29887 48.6 3.0 239585 2 2609525 298877 Caenorhabdi 29887 248.6 3.0 333530 3 26276942 2 26056255 Rattus no 10000 2000 2000 2000 2000 2000 2000 20	49.8 3.0 45210 2 ACUS 754 49.2 3.0 196685 2 ACI12402 49.2 3.0 204456 2 ACC23940 49.2 3.0 20456 2 ACC23940 49.2 3.0 179456 2 ACC05506 48.6 3.0 205429 0 CNSOLRG6	17 50.8 3.1 61052 2 AC123914 18 50.8 3.1 170536 9 AC025593 19 50.8 3.1 170536 9 AC025593 19 50.8 3.1 184425 9 DDRASGG 20 50.8 3.1 184425 DDRASGG 20 50.6 3.1 2418 3 DDRASGG 21 50.6 3.1 219626 10 AC097043	11 53.6 3.3 82392 AC115218 11 53.6 3.2 259782 CNS8CB9 12 52.4 3.2 131665 2 AC115680 13 52.2 3.2 131665 2 AC115680 14 51.4 3.2 30391 2 AC18799 15 51.4 3.2 30391 3 AC187780 15 51.2 3.1 106434 3 AC117074 16 51.2 3.1 106434 AC117074	147.2 9.8 219386 2 AC12235 143.8 8.8 219386 10 875965 141.4 8.7 37892 2 AC117176 141.4 3.3 37892 2 AC118290	16887 9 AC106796 6727 9 AY061638 162948 2 AC015831 162948 2 AC015831 1620 2 AC015831 4 162548 2 AC011583 6 165503 2 AC111518	B ID	ore greater than or equal to the score of the result ore greater than or equal to the total score distribu d is derived by analysis of the total score distribu	

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                    clone RP11-429K17, complete sequence
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       590 CTCAATATGGCATTAGCGTGGAATTAGGTCAGGAGACCTAAGGCTGAACCAAGC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-AUG-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 6, 2002 this sequence version replaced gi:18139346. Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                         TGAATATAATCATTACTATATGACTTTACTTACTTGCATCATCTTCGTTTACTACTACTAC
                                                                                                                                                                                                                                                                                                                CTGACTTTTGGAATGTCATGTATGTTGAACTGGGTCTGAAGACATGGTTTTAACTCAGGC 121127
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    TGTGGGAGATGGGTATTCTCATTTTATAGACAAGGAAATTGACCTCTGGACCTCAGGAAG
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
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DOE Joint Genome Institute.
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Base-by-base quality values are not generally visible GenBank flat file format but are available as part of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RePl1-49K17"
a 37397 c 37923 g 46995
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AUTHORS
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                                                                            TITLE
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Mammalia; Luthefia; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 6727)

1 (Dases 1, Soukhareva, N., Behnam, R., Chang, R., Drews, R., Behnam, R., Chang, R., Drews, R., Theone, H., Hammond, D. and Soukharev, S. target production of Libon, H., Hammond, D. and promoter to target production of recombinant proteins into urine of transgenic animals recombinant recombinant proteins into urine of transgenic animals recombinate r
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(bases | Linton, L. | Nusbaum, C. | Lander, E. | Allen, N. | Anderson, M. |
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Homo.

Birren, B.; Linton, L.; Planta, C. and Lander, E.

Birren, B.; Linton, L.; Planta, C. and Lander, E.

Homo. Saplens, Clone Rpl1-688G24
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All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

All repeats were identified using RepeatMasker:
                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
the reads
contigs. Runs of N are used to separate the reads
and the order in as sequence sampling is useful for
arbitrary. Low pass sequence sampling is useful for
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a overlap it should not be assumed that this clone
will be sequenced to completion. In the event that
will be sequenced to completion in the sort that
the record is updated, the accession number will
be preserved.
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1 1 858 contig of 876 bp in length

1 1834 contig of 876 bp in length

2 1935 1934 gap of 100 bp

1 1835 1936 contig of 876 bp in length

2 1935 2932 gap of 100 bp

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2 1935 2932 contig of 876 bp in length

3 1936 contig of 876

3 1937 2939 of 100 bp

3 1939 contig of 877
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Contact: sequence Information
Content project name: L4338
Center project name: 688_G_24
Center clone name: 688_G_24
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                                                                                                                                                                                                                 CCCTTTTCTCCTGGAGCAGCCTGGCTTCAGATTCTGGCCTCTGCCTTGGCCT------CC 1177
ACCTTTCTGGCTTCAGGTAAGGCTATCTGTAGC
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                                                                    CCTGGGGCAAATGTGTATATATAAGTATGAGGCACA----
                                                                                                       TGGGGGACAGATGTATATATATATATAGATATGAAAGTCACCTACTTGTAAAAAGGATTAATTCT 1532
                                                                                                                                            CCCCCAAGAAAACAATATCAAAAAAACAGAACTAGAGACTAATTGGAGGAGAGATTGCCAG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 620)
Yu,H., Papa,F. and Sukhatme,V.P.
Bovine and rodent tamm-horsfall protein (THP) genes: cloning,
structural analysis, and promoter identification
Gene Expr. 4 (1-2), 63-75 (1994)
95143938
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, D., Gardyna, S., Grant, G., Hagos, B., Haaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Detter B., Connor, T., O'Donnell, P., Detter B., Detter B., Connor, T., O'Donnell, P., Detter B., Connor, T., O'Donnell, P., Detter B., Detter B., Detter B., Connor, T., O'Donnell, P., Detter B., Detter B., Detter B., Connor, T., O'Donnell, P., Detter B., Detter B.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.gene.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L.,
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Homo sapiens, clone RP11-688G24
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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858: contig of 858 bp in length
859 958: gap of 100 bp
959 1834: contig of 876 bp in length
1835 1934: gap of 100 bp
1935 2832: contig of 898 bp in length
2833 2932: gap of 100 bp
2933 3789: contig of 857 bp in length
3790 3889: gap of 100 bp
3890 4780: contig of 891 bp in length
4781 4880: gap of 100 bp
4781 5740: contig of 860 bp in length
5741 5840: gap of 100 bp
5841 6742: contig of 902 bp in length
6743 6842: gap of 100 bp
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------ Project Information
Center project name: 14338
Center clone name: 688_G_24
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26 by 7. Control of 864 bp in length 27791: contig of 864 bp in length 28742: contig of 851 bp in length 28842: gap of 100 bp 29689: contig of 847 bp in length 29789: gap of 100 bp 30642: contig of 853 bp in length 30742: gap of 100 bp 31640: contig of 853 bp in length 1 31740: gap of 100 bp 3 32502: contig of 862 bp in length 1 32602: contig of 862 bp in length 100 bp 3 32702: gap of 100 bp 555 33654: gap of 100 bp 555 34521: contig of 852 bp in length 522 34631: gap of 100 bp 523 4631: gap of 100 bp 52484 3558: gap of 100 bp 5584 3558: gap of 100 bp 100 
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                                                                                                  length
                                                                               Db 153555
                                                                                                                                                                                  Db 153495 CTTTACTGCTANAGNAAACACCCCAGCACCTTGGCACTGCTTTCCCAGTTAATTTCTAAC
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 293; Conserv
                                                                                                                                                                                                                                   1186
                                                                                                                                   1246
1306 GTGACCCCCATGTCAATCATTTGGGGTCTCTACCTATTAGGGAAAAGAACAACCACC 1365
                                                                                                                                                                                                                   CTTTTCAATGACCAAGAAAATCCCCAGGCCCTTGGAATTGTTTACTCAGTTAATTTTCTAAC 1245
                                                                                                                                TAAAGAACCTCTTGTTGCCAAAAGGTATAAAACAGAGCCCTTGTAGCTGTGGGCACAGCT
                                                                                  TATGGAATCTCTTGCTGTTAGAAGTGCGAACAGTGACCTTGTATTTCCGGGCACAGGTGT
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51917 52755; contig of 839 bp

52756 52855: gap of 100 bp

52856 53707; contig of 852 bp

53708 53807: gap of 100 bp

53808 54687; contig of 880 bp
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49928 50027; dan
50028
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66211 67072: contig of 862
67073 67172: gap of 100 2
67173 68036: contig of 864
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17071 47976: contig of
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60408: cont...
0508: gap of
61396: contig of 888 bp 10
61496: gap of
61496: gap of
100 bp
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9574: gap of 100 bp in 10.
60408: contig of 834 bp in 16
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69982: c
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71.8%;
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51816: contig of
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)27: gap of
50871: contig of
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46970: contig of
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contig of 885 bp in length
p of 100 bp
contig of 861 bp in length
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                                                                                                                                                                                                                                                                                             Score 202.4; DB 2;
Pred. No. 2.5e-39;
0; Mismatches 108;
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                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                      1305
                                                                                  153614
                                                                                                                                                                                       153554
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30742: gap of 10 30743 31640: contig of 8 31641 31740: gap of 10 31741 32602: contig of 8t 32603 32702: gap of 10 32703 33554: contig of 8t 33555 33654: gap of 100

29690 29789:

27792 27891:

25981: 25026:

57: gap of 24926: contig of

100 bp 100 bp in

5026: gap of 10 25881: contig of 80 981: gap of 10 26827: contig of 8 5927: gap of 10 5927: gap of 10 7891: gap of 10 7891: gap of 10

1121 gap of 100
122 21995; contig of 874
196 22095; gap of 100 b<sub>1</sub>
16 22965; gap of 870
17 23065; gap of 23967; ccc.

6 18285: gap of 10 6 19098: contig of 8 9 19198: gap of 10 9 20057: contig of 8 8 20157: gap of 10 8 20157: gap of 10

17361: gap of 17361: gap of

51: gap of 1 18185: contig of

100 bp f 824 br

836

15468: gap of 16325: contig of

100 bp 6 857 br

con :: gap of 14419: ccr 10 14519: r

contig of

15368: contig of

11621:

11521

gap of 1 21: contig of

bp in

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bp in

10637: 9673: 8709:

7684: contig of 842 bp 7784: gap of 100 bp 8609: contig of 825 bp

100 bp of 825 bp in

'n

100 L 100 L 100 L 103 gap of 10537: cc-637 Ji Ji contig of continuous co

12566:

.621: gap of 1: 12466: contig of : 1566: gap of 1: 13464: contig of :

f 845 br

in

898

bp in

38356 38455:

14: gap of 1 38355: contig of

100 bp f 841 bp in

2

155: gap of 100 bp 39298: contig of 843 bp 98: gap of 100 bp 40234: contig of 836 bp

bp in

41279 40334: 39398:

contig of 869

34: gap of 1 41179: contig of

'n ĺn 6456 36555:

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Db 153615 GACCCCCAATGTCAATCATTTGGGGTCTCTAGCTATTAGGAAAAAGAACAACAACAACC 153674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
         RENCE 1 (bases 1 to 165503) Addo-Oduola, B., Ali-Osman, F.R., Allen, C., Mary D.M., Adams, C., Arejur, A., Ayele, M., Banks, T., Banboxis, M., Adams, C., Arejur, R., Brown, M., Brown, M., Bonnin, D., Bryant, N.P., Bouck, J., Benton, J., Bencon, E., Brown, M., Bryant, N.P., Bouck, J., Benton, J., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Benton, J., Charles, G.C., Burnel, K.L., J., Charles, C.C., Cayle, M.D., Dadrick, D., David, R., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Carrer, M., Carcer, M., Carcer, M., Chen, A., Chen, 
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Wu,C., Wu,Y., Weinstock,G
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* NOTE: Estimated insert size may differ from sequence length

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence record is

* NOTE: This is a 'working draft' sequence record is

* consists of A contigs. The true order of the pieces

* consists of and their order in this sequence record as

* to not known and their order in the presented as

* arbitrary. Gaps between the contigs are represented unknown.

* arbitrary. Gaps between the contigs are unknown.

* This record will be updated with the finished sequence

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

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Sequencing vector: Plasmid; Dye: 990329
Chemistry: Dye-terminator Blg Dye: 1east 040
Assembly program: Phrap; version 1east 040
Consensus quality: 91433 bases at least 030
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Consensus quality: 97328 bases at least 020
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                                                                                           Submitted (20-JUN-2002) Genome Sequencing Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 219386) McPherson,J.D. and Waterston,R.H.
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Mammalia; Eutheria; Rodentia; Sci
1 (bases 1 to 219386)
McPherson,J.D. and Waterston,R.H.
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AC125147.2 GI:21539180
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Mus musculus chromosome UNK clone
                              Parkway, St. Louis, MO 63108, USA
On Jun 22, 2002 this sequence version replaced gi:21490647
                                               Submitted (22-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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McPherson, J.D. and Waterston, R.H.
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Genome Center ----
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Pred. No. 1.1e-25;
0; Mismatches 118;
                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RP24-350A15, WORKING DRAFT
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Center: Washington University Genome Sequencing Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu

Sequencing Center

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Db 125434 CTTGGGCTTAGGTCTACCTTGTCCTTGCCCAGGTCCAAGAAAAGGCCCAGAACCTTGGCA 125493
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                      1163 CCTCTGCTTGGCCTCCACTTTGTGCTTTTCAATGACCAAGAAAA-TCCCCAGGCCCCTTGGAA 1221
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Consensus quality: 21612 bases at least Q40
Consensus quality: 216506 bases at least Q30
Consensus quality: 216719 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 14.92 in Q20 bases; agarose-fp Quality coverage: 11.97 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; 08
Sequencing vector: plasmid; 1008
Chemistry: Dye-primer ET; 08 of reads
                                                                                                         Similarity
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Insert size: 217980; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
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907..5
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138343. .219386
/note="assembly_name:Contig24"
47433 c 47470 g 62799 t
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80946. .138242
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/db_xref="taxon:10090"
/chromosome="UNK"
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5: gap of unknown length
9: contig of 4363 bp in length
9: gap of unknown length
9: gap of unknown length
9: contig of 11024 bp in length
1: contig of 18158 bp in length
1: contig of 18158 bp in length
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                                                                                                       Score 143.8; DB 2; Pred. No. 7.4e-25;
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of 601 bp in
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                                                                                                 TTCTGGCCTCTGCTTGGCTCCACTTTGTGCTTTTCAATGACCAAG-AAAATCCCAGGCCC
TIGGCACTGCTTTGCCAGTTAATGTCTAACCGAGGAATGTCTTGCTGCCAAAAGGT-GCA
                               TTGGAATTGTTTACTCAGTTAATTTCTAACTAAAGAACCTCTTGTTGCCAAAAAGGTATAA 1275
                                                                 TCCTGCCCCTTTGGTATTTCCACCTTGTCCTTGCCCAGGTCCAAGAAAAAGCCCCAGAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine and rodent tamm-horsfall protein (THP) genes: structural analysis, and promoter identification Gene Expr. 4 (1-2), 63-75 (1994) 95143938
                                                                                                                                                                                                                                                                                                                                                GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 161883] from the original journal article. This sequence comes from Fig. 5.
Location/Qualifiers
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144 c 146 g 167 t
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/gene="THP"
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/db_xref="taxon:10118"
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AC117176 app. 5183817-5221707 strain Dictyostelium discoideum chromosome 2 map 5183817-5221707 strain Dictyostelium discoideum chromosome 2 map 4.00 progress ***, in ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                   gency: Deutsche Forschungsgemeinschaft (DFG).

NOTE: This is a 'working draft' sequence.

NOTE: This is a placed as it is available and this sequence will be replaced.

By the finished sequence as soon as it is available and the accession number will be preserved.

The accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                          /organism="Dictyostelium discoideum"
/strain="AX4"
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4630 c 4690 g 13996
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                                              3.3%;
                                                           Score 54.6; DB 2;
pred. No. 0.0091;
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Rattus.

(bases 1 to 82394) Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Muzny, D.M., Adams, C., Agnartunge, H.C., Agnardam, Bonnin, D., Alsbrooks, S.L., Amaratunge, H.C., Agnardam, B., Bonnin, D., Alsbrooks, S.L., Amaratunge, H.C., Agnardam, B., Brown, M., Bonnin, D., Alsbrooks, S.L., Boule, S., Benton, J., Binage, K., Brown, E., Brown, M.G., Bryant, N.P., Bouck, J., Bowle, S., Berton, B., Brown, M.G., Bryant, N.P., Bouck, J., Bowle, S., Burrell, K.L., Byrd, N.C., Brown, C., C., Condiny, J., Chavez, D., Bouck, J., Bowle, S., Burrell, K.L., Byrd, N.C., Cherler, G., Carroot, L.L., Dederlinh, B., Cherler, M., Christopoulos, C., Cherler, G., Chowdhiry, J., Chavez, D., Bavid, R.C., David, R.C., C., College, M.D., Dathorne, S.R., David, R.C., David, R.C., David, M.C., David, M.C., David, M.C., Deland, C., Exot, F., L., Ding, Y., Durbin, K.J., David, R.C., David, R.C., Ding, Y., David, R.C., Cleveland, C.D., Denn, A.L., Ding, Y., Durbin, K.J., David, R.C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Haber, J., Haylak, P., Hawes, A., Hernandez, J., Harris, C., Haber, J., Dalvet, S., Joudah, S., Carris, R.C., Landry, N., Leal, B., Lewis, L.C., Lawis, L.C., Lawis,
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AC118290 B2394 bp DNA SEQUENCING IN PROGRESS Rattus norvegicus clone CH230-366D18, *** SEQUENCING IN PROGRESS
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Rattus norvegicus; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
Mammalia; Eutheria; Rodentia; Sciurognathi;
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Direct Submission

Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 14, 2002 this sequence version replaced gi:20258108.
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Submitted (15-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 82394)
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NOTE: This is a 'working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of 1
Chemistry: Dye-terminator Big Dye: 100% of 1
Assembly program: Phrap; version 0.990329
Consensus quality: 22144 bases at least Q40
Consensus quality: 24677 bases at least Q30
Consensus quality: 26339 bases at least Q20
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Center clone name: CH230-366D18
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Rattus.

Rattus.

Rattus.

Rattus.

1 (Dases 1 to 259782)

Manmalia; Butheria; Kouchard Rattus.

1 (Dases 1 to 259782)

Manualia; Butheria; Rough Rattus, Ayele, M., Banks, T., Brown, M., Bryant, N.P., Barboroks, S. R., Land, M., Brown, E., Brown, M., Bryant, N.P., Barboroks, S. R., Land, M., Bryant, N.P., Barbaria, J., Barboroks, S. R., Charistopoulos, C., Bautheria, M.L., Byrd, N.C., Butheria, M.C., Byrd, N.C., Coyle, M.D., Dathorne, S. R., David, R., Chen, G., Chen, Z., Chen, A.L., Dathorne, S. R., David, R., Chen, G., Chen, Z., Chen, A.L., Ding, Y., Durbin, K.J., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S. R., David, R., Chen, G., Chen, A.L., Ding, Y., Durbin, K.J., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S. R., David, R., Chen, G., Chen, A.L., Ding, Y., Durbin, K.J., Davila, R., David, R., Chen, A., Carner, T., Call, R., Frantz, P., Davila, M.L., Davis, C., Edwards, C.C., Elhaj, C., Escotto, M., Pagado, O., Denn, A.L., Ding, Y., Durbin, K.J., Frantz, P., Davila, R., Carroll, J., Coyle, M., Pord, J., Coyle, R., Martine, S., Hamilton, K., Garcia, A., Garner, T., Hawes, A., Hanliton, K., Garcia, A., Garner, T., Hawes, A., Hallins, B., Gorrell, J., Harris, K., Hart, M., Holloway, C., Hallins, B., Garner, M., Havelak, P., Hawes, A., Holloway, C., Hodsh, S., Hollows, C., Lewis, L., Jackson, L.E., Jackson, L.E., Jackson, L.E., Jackson, L.E., Jackson, E., Kell, S., Harly, S., Hanne, J., Lauder, S., Hally, S., Hanne, J., Kovar, C., Lewis, L., Lucler, R., Martinale, A., Martinez, E., M., Keller, M., Ke
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AC115218 regions clone CH230-2D5,
Rattus norvegicus clone CH230-2D5,
46 unordered Pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC115218.4 GI:21953463
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/db_xref="cH230-365D18"
/clone="CH230-365D18 t 6652 others
15538 c 15669 g 21068 t
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pred. No. 0.015;
0; Mismatches 97; Indels 0;
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PNA SEQUENCING IN PROGRESS ***,
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Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Scherer, S., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Tang, H., Sodergren, E., Sonaike, T., Sparks, A., Tamerisa, R., Tamerisa, R., Thomas, S., Sutton, A., Taylor, C., Taylor, T., Telfrod, B., Vinson, R., Wang, Q., Taylor, C., Taylor, T., Villaion, D., Wang, Q., Wansey, J., Vasquez, L., Warren, R., Washington, C., Warlington, S., Warren, R., Wang, S., Ward-Moore, S., A., Wleczyk, R., Wooden, S., Worley, K., Wulliams, G., Wu, T., Zhou, J., Zorrilla, S., Nelson, D., Wu, C., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Neinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: Estimated insert size may differ from sequence length (see http://www.hgss.bcm.tmc.edu/docs/genbank_draft_data.html)

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* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

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Contact: hgsc-help@bcm.tmc.edu
contact: project Information
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Center project name: CH230-2D5
Center clone name: CH230-2D5
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4061
5076
5176
6190
6290
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7783
9904
11217
11317
11317
11317
14164
                                                                                                6189: control unknown length 6289: gap of unknown length 7682: contig of 1393 by in length 7682: contig of 1020 bp in length 8802: contig unknown length 9903: contig of 1001 bp in length 10013: gap of unknown length 11216: contig of 1213 bp in length 11316: gap of unknown length 12178: contig of 1462 bp in length 12778: contig of 1462 bp in length 12878: gap of unknown length 14633: contig of 1462 bp in length 14633: contig of 1462 bp in length 14633: contig of 1462 bp in length 14633: contig of 1185 
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of 1223
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	000000000000000000000000000000000000000	contig of 14542 bp 1m contig of unknown length gap of 14602 bp in contig of 14602 bp in gap of unknown length gap of unknown length contig of 14743 bp in gap of 14743 bp in	105607: Yer of 9006 bp 11.14613: Contig of 9076 bp 11.14713: gap of unknown lengt 114713: gap of unknown lengt 127391: contig of 12678 bp 117491: gap of unknown 127491: gap of 10773 bp 1138264: contig of 10773 bp 1138264:	contig of 8295 bp in contig of unknown length of 9196 bp in contig of 9196 bp in contig of unknown length	contig of lengt gap of unknown lengt contig of 4896 bp in gap of unknown lengt gap of unknown lengt contig unknown lengt	67017: contig of 3013 length 67017: gap of unknown length 67117: gap of unknown 2010 71839: contig of 4722 length 71939: gap of unknown by in	55434: CONCLY Unknown 55534: gap of unknown 61098: contig of 5564 61198: gap of unknown	46894: CULLY 4233 46794: gap of unknown length 6695 50840: Contig of 4046 bp in length 66795 50840: Gap of unknown length 66795 50940: gap of unknown length	contig of 3964 bp in contig of unknown lengt gap of unknown lengt	82: contig of unknown lenges gap of unknown lenges contig of 1984 bp 166: gap of unknown lenges gap of unknown lenges contig of 2122 bp 188: contig of unknown lenges conti	30276: contry Thrown length 30376: gap of unknown length 32725: contry of 2349 bp in length 32825: gap of unknown length	contiguinknown lengt gap of unknown lengt from the contiguinknown length gap of 1763 bp in	contil of length gap of unknown length contil of 1376 bp in length contil of unknown length gap of unknown length	0: contrag unknown length 0: gap of unknown length 7: contig of 1427 bp in length 17: gap of unknown length 17: gap of unknown length	gap of unknown length contig of 1079 bp in length gap of unknown length gartin of 1535 bp in length		us-09-000
-	*****	300 861 110 861	cont from Cont 1666	COMMENT IMPORT TEPT			Sperma Sperma Ehrhart La (bas REFERENCE 1 (bas REFERENCE Choisn	WSIN		RESULT 13 CNSO8CB9 CNSO8CB9 CNSO8CB9 COUST CNSO8CB9 DEFINITION CNSORES	Qy 291 TGATAAGA 270               6938 Db 6931 ATATAAAA 6938	Qy 231 AATAGTAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	OY 171 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Db 6751 ABABABABABABABABABABABABABABABABABABAB		BASE COUNT 69773 a 5	
	the a	32083 bp contig from 12025 to 130636 32083 bp contig from 120737 to 131665. 10929 bp contig from 120737 to 131665. 10929 bp contig from 120737 to 131665.  * NOTE: This is a 'working draft' sequence of the pieces  * consists of 6 contigs Gaps between the of the sizes  * consists of 6 contigs of N. The order of the sizes  * consists of 6 contigs of N. The order of the sizes  * consists of 6 contigs of N. The order of the sizes  * consists of 6 contigs of N. The order of the sizes	continue. The sequence of phage, etc.  continue. The sequence of phage, etc.  from E. coll. yeast, vector, phage, etc.  from E. contig from 1 to 16662  Contigs composition:  1 to 16662 bp contig from 16763 to 23333  16662 bp contig from 16763 to 79741  6571 bp contig from 23434 to 79741  6571 bp contig from 23434 to 7111924	IMPORTANT: This sequence.  IMPORTANT: This sequence and the release of the work represent the correct sequences and the release of the vork represent the sequence is in progress and the release of the represent the sequence may change as work on the sequence that the sequence with foreign sequence work on the understanding the contaminated with foreign sequence has ed on the understanding the contaminated with foreign sequence.	1155 102- 106 E	i gr	Sperime CF. 1 (13665)  Birhartoideae; 013665)  1 (bases 1 to 131665)  1 (bases 1 to 131665, Cattolico, L., Demange, N., Wincker, F., Choisne, N., Orjeda, G., Cattolico, L., Salanoubat, M., Choisne, N., Orjeda, G., Scarpelli, C., Salanoubat, M., Choisne, N., Orjeda, G., Scarpelli, C., Salanoubat, M., Choisne, N., Orjeda, G., Scarpelli, C., Salanoubat, M., Choisne, N., Orjeda, G., Cattolico, L., Scarpelli, C., Salanoubat, M., Choisne, N., Orjeda, G., Cattolico, L., Company, C., Cattolico, L., Company, C., Cattolico, L., Company, C., Cattolico, L., Company, C., Cattolico, L., Cattolico, L., Cattolico, C., Cattolico,	iva iva Viridiplanta hvta; Magnolio	7.1 GI:22208188 GS PHASE2; HTGS_ACTIVEFIN.	Inear HTG 09-ANG-200- 131665 bp DNA linear HTG 09-ANG-200- CNSO8CB9 Chromosome 12 clone OSJNBb0101110, *** SEQUENCING IN DOTYZE Sative Chromosome 12 clone OSJNBb0101110, *** SEQUENCING IN		AATAGTAAUGHATTAAAAGAGAAAAAAAAAAAAAAAAAAA	ARARARACE 1 111   1   1   1   1   1   1   1   1	AGAAAAAAAAAAAAAAAAAAATTTTTTTATTTTANNAAAAWAAAAAAAA	tch 53.7%; pred. No. 87; Inders 101; Conservative Mismatches 170 101; Conservative Hill Hill 101; Conservative Hil	5782 g 68502 C F SCORE 52.4; DB 2; I	

30377 32826 32826 32826 32883 35883 37867 40089 40189 44153 44253 46695 46795 46795 50841 55435 55435 61099 61199 61199 61199 61199 61199 671840 771840 771840 77185 82255 82255 8235 8235 8436 87318 87317 87317 87317 87317

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                                                                                                                       Direct Submission
Submitted (22-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
                                                                                                                                                                                                                                                                                                                                                                                                      Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K., Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and Noegel,A.A.
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Dictyostelium discoideum chromosome
AX4, *** SEQUENCING IN PROGRESS ***,
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Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 59004)
                                                                              (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
                                                                                                                                                                                                                                                                                                                          The Dictyostelium Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                            Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE2
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                                                    (http://www.uni-koeln.de/dictyostelium/project.shtml
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112025 120636: contig of 8612 bp
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120737 131665: contig of 10929 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79842
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: Deutsche Forschungsgemeinschaft (DFG)
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/cultivar="Nipponbare"
/sub_species="japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="OSJNBb0101110"
/clone_lib="OSJNBb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 131665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="Folate-11ke transporter 3."
/product="ALI92631.1"
/protein_id="ALI92631.1"
/db_xref="GI19683008"
/translation="MEDSDKENTLLLPNNKYRNONFIRNODEDENENENDDNENDDN KRNYISINNYEPYKEIDNNNKNNNNNIINNNKINFYNNLIPRIKSYFOEIKPFLK
YCSFSFLFSEDPSEPYLVDYFTNVLGINOTIVYOEIKPYWTYSYFVFLLIFGILGEII
GYKVIIIIGMAKIIIGVLLSTNNIIMMILEQITEGLSYSAYTVELAXIYFSLDTSE
YOKMACRYNAGYLVGIVSSGLLGOLLVEORLDLVYLLSIACGTNILALIGHIGNIK
                              KDRKENNIEWEPRLFKKVNDQWIYKYQNHTLYDQNEPKEIETDGIIHFEGTLIKKESK
QNLVEKCGASENEIIV"
                                                                                                         /translation="meigtsstinnigvaptipodivnnnnhnnnssnnssnnnsiss spidssqlmngrostpssppieevleeeprnllisllselkigvdlsrvplptfile prsllekfidnmihgeilcnlsklespmdrmhllitkwilsafhyrkglqkpryntpilg eifftemekeftensmihgeilcnlsklespmdrmhllitkwilsafhyrkglqkpryntpilg eifftemekeftensmihgeilcnlsklespmdrmhllitkwilsafhyrkglqkpryntkensmiftenskelgnsm avivdgsstitllgqeeryitfptavargiifgtlltelygnstisckqtnikvemd fkakpmfggeynvvcgkikkgnetthffngkmdkkveitlsssssskkkngstndil
                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAL92634.1"
/db_xref="GI:19683011"
                                                                                                                                                                                                                                                                                                                                                                               complement(join(8529. .8670,8749. /note="ORF_ID:dd_00320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSLSPTITSLYLNEGFNQPITTEILSSCKNLKNLYMYDIKQPLFLNDDDDDFNLSIES
IHLMPGFNQILKNGNLLKFGFKNLYIYDINQPLIPNESIIPNNNNNNNNNNNNNNNNNNNN
NNNYNINLLHISGNYKFKLSKGIIPSNSNTKISNLYIGNLNEPLIPNESIPNNVESLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSIEPKTFQYYKHTFSIYYDGWEIPDDIENLALGEGIDLDNLII
PDTVECLLLMDGFDKEIKEGFISDTINELFILDIKQPLSIGSIGESILMLEFGDGYNH
PITKGIIPNSVECLYLRAIKKELSNDSIPNSIEKLYLVDGFNQNLSFILTSSSTSTSSL
KNLYIYNIGNNILNIGSIPNTIKLLYFGDGFNETILPNLIPPNVNTLYLRDIKKALIK
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VKSEIFSATGDSTLVLDEIYSATGDSTIPV"
Join (8804. 6831,8914. 8259)
/note="ORF_ID:dd_00322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISTSVNGDDNVGAAITGSGGVSGSGSGSVVDVKDNGDVKAAITGSGGVSGDDDVKAAI
TGSGGVSGSDDVVKAAITGSGGVSGSGRGSVVDVKDNGDVNAAITGSGGVSGSGSTIP
VMAAITGTGSSGSGTTIPVKSEVFSATGDSTIPVLEDVQAAITGSGGVSGSGSGSGSVVD
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SFIIYNCCFEFVSPIVNVQIAKKLSSRIGVLFSENIMVALTIQVLVQSAVGKQFLNLD
IKTQFYYYGACLFFLSFGEAILFGFLFLKKKINSNSNSNVDVLIVNHNTQNQNSEE
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2401. .2490,2566. .2964))
/note="ORF_ID:dd_00311"
                                                                                   WDCNDAVKTQMITRQISEQEEFESQRLWQKVSHAIIKKNQKDATFEKNKLEDEQRKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGSGYQFKITSDLIPPSVLNLYLYDINEPITNESIPKTLKTIYISSQYEHPINNLISK
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/product="hypothetical
/protein_id="AAL92633.1
/db_xref="GI:19683010"
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/protein_id="AAL92632.1"
/db_xref="GI:19683009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(4543. .4746,5110. .6003)
/note="ORF_ID:dd_00324"
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                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTKLSSVGLLSLVGVSLVAGDHYSCDQMKKLSHEYFPESVADNM
ICLSFHSSGWNSISNTKNSIGLWYKLMHNVAEMVYTEFGYNHWDAWNKGKCNGWNQCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDQKFSLKEVISDLFGTFKNADIVRWYIWSGIAISIHQIVITYWQNLFFQVNDDQSWN
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DQKVTNTSDTVELEKSLNNNASFKEFDPEVSPEFERVVSDF11LDEDDQDSTPPPY1D
SGNNNTTTATTTEDVDALYKEQFLLRQQQS1FDQ1LRQRQLEQQ11QQQQEQQQQDQQ
                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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/db_xref="GI:19683014"
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DNIEALVKSRQYVPSYDKSKN"
Join(19036. 19152,19298. .19672,19768. .20136)
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/translation="MQNKPSFILNUPSANKGLLPPKVESLQEQSDRALSQETSFNTNL
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TRTLFYIIDSGTNTKKYLEDKYYLGERHPRIPDSEYYPLVDEFLAAAFNKWPKVIVQF
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/protein_id="AAL92639.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNIDKARVKTLKSSGCSNSFGSFESTYPANLHGTMDDFEFKTTI
KRINAKCNFVLSKKYYLVFLISLVGLILVIVGFTKSAKSVNSAGGFREDAFKQNNLND
FSIGFSDNRSEDFNNNNNYDDDDDSSPSRFYGGFFYFIALGFALMFLGCCIFGISFAK
FRNKVLNKIRDELVAVNKHFNARGITWNLESEVVRKYIPRHEYNGHKNNQAYRNSIKY
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TAEQAYQWTDGRCIFASGSPFKPVEYKGKTFVPGQGNNMYIFPGLGLAASVCEAKHVT
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GSAGIGVADCIMSLFDEAGVSKEEARKSFWFVDSKGLITTTRGDELTSQKKQYAREDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(15996. .16044,16634. .18174)
/note="ORF_ID:dd_00315"
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IGQVLNSTIYCFSFYFFGLN"
                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                          NNNNNNKNNIQDEKGICINVDELKNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAL92638.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(20613. .20705,21176. .21646)
/note="ORF_ID:dd_00312"
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/protein_id="AAL92635...
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Best Local Sim
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TITLE
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Mammalia; Eutheria; Rodenti
1 (bases 1 to 303091)
DOE Joint Genome Institute.
Sequencing of Human Chromos
Center: Joint Genome Institute Center Code: JGI
                                                             Submitted (17-NOV-2000) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACO84799 303091 bp DNA linear I
Mus musculus chromosome 16 clone RP23-197M9, WORKING
SEQUENCE, 101 unordered pieces.
                                                                                          Direct Submission Submitted (17-NOV-2000)
                                                                                                                                     2 (bases 1 to 303091)
DOE Joint Genome Institute.
                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                        Mus musculus
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HTG; HTGS_PHASE1; HTGS_1
                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                  AC084799
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                                             -Genome Center
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27087. .27299
/note="ORF_ID:dd_00321"
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TNIAFDESSLPAVQYFYKVSISNQPLINSNSYIKSFMYNVDSCNENEVTNIQYFSNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYKGTWCIEIKSGDHNQLQVIRIETNGGSDKPSGDLSM"complement(25915, .26583)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAIEKSTSRPSSYYCSASNQPYTYYCSIWGCGPSYTSANCQQINSTSPTLINENNYYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYYLLLPSSDQFLLYQMVGYIVLKNNATTGDIVLESHKRMSEHIGGQVTLTPGETQTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAIKFFTGGFVSSVEKPTNTLKTENKLTGNGLVLGEDLNQQDIYYNEDEEQVQLYNNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAEVETKSDFENIKYRTIYVPMYKLTYHYNNRDYMFVINGQNGKSHGIRPYGAGSIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.2%;
                                                                                                                                                                                                                                                                                                                                                                       HTGS_DRAFT
                                                                                                                                                                                                                                                                        Chordata;
Rođentia;
                                                                                                                                                                                                          Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51.4; DB pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o.1"
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Sciurognathi; Muridae;
                                                                                                                                                                                                            16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 59004;
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                                                                     Facility,
Creek, CA
                                                                                                                                                                                                                                                                                                     Euteleostomi;
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                                                                  DOE Joi
1 94598,
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                                                                       Joint
98, USA
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Wed Feb 19 14:09:20 2003
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consensus quality: 17579 bases at least Q20
consensus quality: 186949 bases agarose-fp estimation
estimated insert size: 293091; sum-of-contigs estimation
estimated insert size: 19300; squarose-fp estimation
consists coverage: 3.28 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence It currently
quality coverage: 3.28 in Q20 bases; sum-of-contigs estimation.

* Note: This is a 'working draft' sequence of the pleces
consists of 101 contigs. The true order of the pleces
consists of 101 contigs. The true order of the pleces
consists of 101 contigs. The true order of the pleces
consists of 101 contigs. The true order of the pleces
consists of Nowm and their order in this sequence record is
consists of Nowm and their order in this gaps are unknown.

* This record will be updated with the finished sequence
consists of Nowm and the sacet sizes of the gaps are unknown.

* This record will be updated with the finished sequence
consists of Nowm and the sacet sizes of the gaps are unknown.

* This record will be updated with the finished sequence
consists of Nowm and the sacet sizes of the gaps are unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9244
10493
10593
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118473
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119553
21013
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1216: gap of unknown length
2536: contig of 1320 bp in length
2636: gap of unknown length
4057: contig of 1421 bp in length
4157: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17825: gap of unknown length
9143: contig of 1318 bp in length
9243: gap of unknown length
10492: contig of 1249 bp in length
10592: gap of unknown length
11666: contig of 1074 bp in length
11766: gap of unknown length
11766: gap of unknown length
12950: contig of 1184 bp in length
13050: gap of unknown length
14285: contig of 1235 bp in length
14285: contig of 1235 bp in length
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4257: gap of unknown length
5245: contig of 1088 bp in length
5345: gap of unknown bp in length
6461: contig of 1116 bp in length
6561: gap of unknown length
6561: gap of unknown length
7725: contig of 1164 bp in length
   10//y: coulty unknown length
18378: gap of unknown length
18378: gap of unknown length
19452: contig of 1074 bp in length
19552: gap of unknown length
201012: contig of 1074 bp in length
211012: gap of unknown length
22169: gap of unknown length
22169: gap of unknown length
23367: gap of unknown length
23467: gap of unknown length
23467: gap of unknown length
24559: contig of 1092 bp in length
24559: gap of unknown length
25825: gap of unknown length
27036: gap of unknown length
27036: contig of 1111 bp in length
27036: contig of 1111 bp in length
28345: gap of unknown length
29556: gap of unknown length
29556: gap of unknown length
30883: gap of unknown length
30125: contig of 1127 bp in length
3125: contig of 1172 bp in length
33397: contig of 1172 bp in length
334645: contig of 1172 bp in length
334645: contig of 1174 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13950: contig of 1184 bp in le 13950: gap of unknown length 14285: contig of 1235 bp in le 14385: gap of unknown length 1578: contig of 1093 bp in le 1578: gap of unknown length 1579: contig of 1201 bp in le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 bp in 1-
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40953
42117
42217
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43473
446704
44704
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471275
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49970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34745:
35894:
35994:
37156:
37256:
38396:
                                                                                                                                                                                                                          bauda: coulty without length
58922: gap of unknown length
60547: contig of 1025 bp in length
60647: gap of unknown length
61843: contig of 1096 bp in length
61843: contig of 1096 bp in length
6298: contig of 1125 bp in length
64220: gap of unknown length
64220: gap of unknown length
65298: contig of 1078 bp in length
65498: contig of 1078 bp in length
65408: gap of unknown length
65762: contig of 1264 bp in length
66862: gap of unknown length
66802: gap of unknown length
69102: contig of 1275 bp in length
69400: contig of 1275 bp in length
69400: contig of 1275 bp in length
70718: contig of 1278 bp in length
70718: contig of 1279 bp in length
70818: gap of unknown length
70818: gap of unknown length
71995: contig of 1177 bp in length
71995: gap of unknown length
72332: gap of unknown length
74476: contig of 1137 bp in length
74576: gap of unknown length
74563: contig of 1138 bp in length
75963: contig of 1138 bp in length
75963: gap of unknown length
77021: gap of unknown length
77121: gap of unknown length
7812: contig of 1091 bp in length
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54020: gap of u
55101: contig o
55201: gap of u
5524: contig o
56324: contig o
57583: contig o
57683: gap of u
57683: gap of u
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of of 1470 bp in length
of unknown length
of of 125 bp in length
of of 1066 bp in length
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ig of 1130 bp in length
of unknown length
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unknown length
of 1131 bp in length
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of 1150 bp in length
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f unknown length
g of 1287 bp in length
g of 1058 bp in length
g of 1058 bp in length
g of 1059 bp in length
of unknown length
of unknown length
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ig of 1112 bp in
ig of 1033 bp in length
ig of 1093 bp in length
of unknown length
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E unknown
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3.2%;
Query Match
Best Local Similarity 52.0%;
Matches 115; Conservative
Search completed: February 17, 2003, 15:35:06
Job time : 5250.6 secs
                                                                                                                                                                    171 AAAAAAAACATTCTTATGGGGGATAAACGGCCAAAGGATACAAACAGTTCAGAAAAGAATA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81804: contig of 1087 bp in length
81904: gap of unknown length
83007: contig of 1103 bp in length
83007: contig of 1060 bp in length
84167: contig of 1060 bp in length
84267: gap of unknown length
85347: contig of 1080 bp in length
85447: gap of unknown length
86521: contig of 1074 bp in length
86521: dantig of 1074 bp in length
86521: dantig of 1123 bp in length
8774: contig of 1075 bp in length
87844: gap of unknown length
87844: gap of unknown length
87865: contig of 1121 bp in length
89865: contig of 1121 bp in length
99065: gap of unknown length
99067: contig of 1111 bp in length
990176: contig of 1111 bp in length
                                                                                                                                                                                                                                                                                                                                                   96211: gap of unknown length
98351: contig of 2141 bp in length
98452: gap of unknown length
99645: contig of 1193 bp in length
99745: gap of unknown length
                                                                                                                                                                                                                                                                                                   ; Score 51.4; DB 2; Length 303091; pred. No. 0.05; 0; Mismatches 106; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      known length
1003 bp in length
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1077 bp in length
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bp in length
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Title:

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4, Appli
4, Appli
70, Appli

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Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Sequence:
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length:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is the number of results predicted by chance to have ater than or equal to the score of the result being pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-629-643A-5
US-09-155-884-5
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US-09-022-255-1
US-09-022-256-1
US-09-022-253-1
US-09-022-253-1
US-09-022-257-1
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US-08-845-258-45
US-08-990-571-45
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US-08-723-142A-7
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US-08-232-463-14/c
                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPACE: (703)883-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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 Query Match
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FILING DATE:
FILING DATE: 26-AUG-191
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.76
REFERENCE/DOCKET NUMBER: 3
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.:
CURRENT APPLICATION DATA:
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ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G
                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                             TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lir
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CITY: Alexandria
STATE: VA
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22313-0299
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US-08-487-685-4
US-08-486-013-70
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US-08-486-013-70
US-08-342-268-70
US-08-36-135-9
US-08-36-135-13
US-08-36-135-13
US-08-36-135-15
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 Score 86;
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 Length 7218;
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Pred. No. 2.2e-15;

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RESULT 2
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                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/629,643
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: VIKSINIS, Ann S
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 150.167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lee, J. L.
APPLICANT: Lee, N. A.
TITLE OF INVENTION: IL-5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 612-359-3260
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                                                                                           612-359-3263
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single
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RESULT 4
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US-09-280-799-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 1
LENGTH: 6727
                                                                                                                                                           Sequence 5, Application US/09155884
Patent No. 6215040
GENERAL INFORMATION:
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Best Local
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/280,799
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEO ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL TITLE OF INVENTION: TRANSDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dean, Nicholas M. APPLICANT: Karras, James G APPLICANT: McKay, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                           APPLICANT: James J.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                           2593
                                                                                                                                                                                                                                                                                    1982
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                                                                                                        CORRESPONDENCE ADDRESS:
                                                     STREET: F. CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide
LOCATION: 650...3771
OTHER INFORMATION: Join 650...730,
OTHER INFORMATION: 3468..3596, 36
                          COUNTRY: UZIP: 55402
                                                                                            ADDRESSEE:
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                                                                               E: Schwegman,
P. O. Box 2938
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IL-5 TRANSGENIC MOUSE
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3676..3771
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FILING DATE: 7
CLASSIFICATION:

7 AUGUST 1995

USSN 08/410,535

PRIOR APPLICATION DATA:

FILING DATE:

21 MARCH 1996 JMBER: USSN 0 7 AUGUST 1995

FILING DATE: 21 MAN APPLICATION NUMBER:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

USSN 08/620,694 CH 1996 USSN 08/538,765

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US-09-022-696-1/c
US-09-022-696-1/c
Sequence 1, Application US/09022696
Patent No. 6072037
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; LOCATION:
US-09-022-255-1
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Best Local Similarity
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                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                          2803
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1839 GATCCTTATATCTACACTCTCAAGTGCCCAGATTATAAGTGTGTGCACCACTATACTCAGTT 1898
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    2922 GATCATCAAGTCTCAGTTCCCAAGTGCTGGGACTTCAGGTATACAACACTAT-GTCAGAT 2864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
              CURRENT APPLICATION DATA:
                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLECULE TYPE:
                                                                                                                                                                                                                                PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTI-SENSE:
                         COMPUTER: Apple Power macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
                                                                                                                              STREET: 51 Un:
CITY: Seattle
STATE: WA
                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                      E: Immunex Corporation
51 University Street
                                                                                                                                                                                                  Yao, Zhengbin
Spriggs, Melanie
Fanslow, William
NYENTION: No. 6072037el Receptor That Binds IL-17
SEQUENCES: 10
                                                                                                              USA
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121..2715
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us/09/022,696
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Pred. No. 3.2e-07;
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                             Version 6.0.1
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                                                                                                                                                                                                                                                                                    RESULT 8
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                                                                                                                                                                                                                             Sequence 1, Application US/08978773 Patent No. 6083906 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            2803
           COMPUTER: Apple PowerMacIntosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft word for PowerMacIntosh,
CURRENT APPLICATION DATA:
                                                              ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                       1959
                                                                                                                                                                                                                                                                                                                                                                                 2863
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HYPOTHETICAL: N
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                                                                                                                                                                                       TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206)587-0430
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APPLICATION NUMBER:
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APPLICATION NUMBER:
                                                                                           COUNTRY: U
                                                                                                                                STREET: 51 Un:
CITY: Seattle
                                                                                                                        STATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: HVS13 receptor
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                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3288 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                            104;
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                                                                                                                                                51 University Street
                                                                                                         USA
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                                                                                                                                                            Immunex Corporation
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                                                                                                                                                                                                  Method of Regulating Nitric Oxide Production
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US/08/978,773
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34,695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                          Version 6.0.1
                                                                                                                                                                                                                                                                                                                            2761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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ARPLICATION UMBER: USSN 60/0:
ARPLICATION NUMBER: 1996
FILING DATE: 27 NOVEMBER 1996

USSN 60/052,525

CLASSIFICATION:

FILING DATE:

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REFERENCE/DOCKET NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
REFERENCE/TON INFORMATION:
TELEPOME: (206)587-0430
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE
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Best Local Similarity 63.8
Conservative
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                         Sequence 1, Application of the patent No. 6100235 patent No. 6100235 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          1839 GATCCTTATATCTACACTCTCAAGTGCCCAGATTATAAGTGTGCACCACTATACTCAGTT 1898
                                                                                                                                                                                                                                                                                                                  2922 GATCATCAAGTCTCAGTTCCCAAGTGCTGGGACTTCAGGTATACAACACTAT GTCAGAT 2864
                                                                                                                                                                                                                                                                                          ORGANISM: Mouse
STRAIN: HVS13 receptor
                                                                                                                                                                                                                                                                       APPLICANT: YAO, ZIENA APPLICANT: Spriggs, APPLICANT: Fanslow, APPLICANT INVENTION:
                                                                                                         CORRESPONDENCE ADDRESS:
ZIP: 98101...
ZIP: 98101...
ZIP: 98101...

COMPUTER READABLE FORM: 115k

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Apple Power Macintosh

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                    STREET: 51 0H-
CITY: Seattle
STATE: WA
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                                                      WAUSA
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                                                                                          E: Immunex Corporation
51 University Street
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                                                                                                                                                                         Zhengbin
                                                                                                                                             No.
                                                                                                                                                      Melanie
William
                                                                                                                                                                                                                                                                                                                                                                                                 score 58.2; Di
pred. No. 3.2e
0; Mismatches
                                                                                                                                             6100235el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                ); DB 3; Length 3288;
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US-09-022-260-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
ABROTH: 3288 base pairs
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Query Match
Best Local Similarity 63.8
Matches 104; Conservative
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                                                                                                                                                                                                RESULT 11
US-09-022-259-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                            1839 GATCCTTATATCTACACTCTCAAGTGCCCAGATTATAAGTGTGCACCACTATACTCAGTT 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFERENCE/DOCKET NUMBER: 26
ECOMMUNICATION INFORMATION:
ELEPHONE: (206)587-0430
ET PER CONTROL (206)587-0430
                                                                                                                                                                                                                                                                                                                                        1899 ТАТССТСТБСТВАССВАСТВАССССВАТТАТАСАЛАСАСАСАСАТАТАТАСАСАСАТАС 1958
                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           ORGANISM: Mouse
STRAIN: HVS13 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ME: Perkins, Patri
GISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                             2803 ACACGCACACACACACACACACACACACACACGCACA 2761
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APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION NUMBER: USSN 08/410,535
IG DATE: 23 MARCH 1995
                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFICATION:
                                                                                                                 APPLICANT: Yao, AMERICAN PERIODS IL-17
APPLICANT: Spriggs, Welanie
APPLICANT: Fanslow, William
APPLICANT: NO. 6191104el Receptor That Binds IL-17
APPLICANT: NO. 6191104el Receptor That Binds IL-17
APPLICANTION: NO. 6191104el Receptor That Binds IL-17
APPLICANTION: NO. 6191104el Receptor That Binds IL-17
APPLICANT SPRIME STATEMENT OF INVENTION: 10

TITLE OF INVENTION: 10
COMPUTER READABLE FORM:
MEDIUM TYPE Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                   ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                              No.
                                                STREET: 51 000
CITY: Seattle
STATE: WA
                         COUNTRY: U
                                                                                                                                                                              , Application US/09022259 6191104
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                                          USA
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                                                                                                                                                             zhengbin
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 58.2; DB 3; Length 3288; pred. No. 3.2e-07; pred. No. 3.2e-07; Mismatches 58; Indels 1;
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US-09-022-259-1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION
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Best Local Similarity
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                                                                                                                                                                                                                              RESULT 12
US-09-022-257-1/c
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MOLECULE TYPE: CDI
MOLECULE TYPE: NO
HYPOTHETICAL: NO
ANTI-SENSE:
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                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                    NUMBER OF SEQUENCES:
                                                        CITY: Seattle
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
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121..2715
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TELEFAX: (200)
INFORMATION FOR SEC ID NO: 1:
SPOURNCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
LENGTH: 1316 acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Power Macintosh 7.5. OPERATING SYSTEM: Apple Operating System 7.5. SOFTWARE: Microsoft Word for Apple, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: PETKINS, PARTICIA

NAME: PETKINS, PARTICIA

REGISTRATION NUMBER: 326

REFERENCE/DOCKET NUMBER: 266

REFERENCE/TON INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION (206)587-0430
                                                                                                                     Sequence 1, Application US/09022257 Patent No. 6197525
                                                                                                                                                                                                                                                                                                                                 1839 GATCCTTATATCTACACTCTCAAGTGCCCAGATTATAAGTGTGCACCACTATACTCAGTT 1898
                                                                                                                                                                                                                                                                                                                 2922 GATCATCAAGTCTCAGTTCCCAAGTGCTGGGACTTCAGGTATACAACACTAT-GTCAGAT 2864
                                                                                                                                                                                                                                                                                      ORGANISM: Mouse
STRAIN: HVS13 receptor
                                                                                                                                                                                                       2803 ACACGCACACACACACACACACACACACACACGCACA 2761
                                                         APPLICANT: Yao, Zhenye, AppliCANT: Sprigs; Melanie AppliCANT: Sprigs; Melanie AppliCANT: Fanslow, William AppliCANT: Fanslow, No. 6197525el Receptor That Binds IL-17 TITLE OF INVENTION: 10
                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA to mRNA
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pred. No. 3.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          58;
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COMPUTER: Apple Power Macintosh System 7.5.5 OPERATING SYSTEM: Apple Operating System 6.(
SOFTWARE: Microsoft Word for Apple, Version 6.(
SOFTWARE: Microsoft Word for Apple, Version 6.7
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
US-09-022-257-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: DATA: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EILING LATER OF CLASSIFICATION DATA: CLASSIFICATION DATA: USSN 08
PRIOR APPLICATION NUMBER: USSN 08
APPLICATION NUMBER: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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Query Match 63.8%;
Best Local Similarity 63.8%;
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                            US-08-845-258-7/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                  Sequence 7, Application of the patent No. 6183976 patent No. 6183976 general INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1839 GATCCTTATATCTACACTCTCAAGTGCCCCAGATTATAAGTGTGCACCACTATACTCAGTT 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: HVS13 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                        APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS: BERRY ADDRESSEE: SEED AND BERRY 701 Fifth Avenue ADDRESSEE: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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121..2715
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ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: PLOPPY disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: STEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-258

CONTWARE: PATCHION REALOSE: US/08/845,258

CURRENT APPLICATION 24-APR-197

FILTHG DATE: 435

CLASSIFICATION: 24-APR-197

TELEPY/AGENT INFORMATION:

REGISTRATION INUMBER: 210121.4:

REGISTRATION UNMBER: 210121.4:

REGISTRATION INUMBER: 210121.4:

REGISTRATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-6031

TELEPHONE: (206) 622-6031

TELEPHONE: (206) 622-6031

TELEPHONE: CARRACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

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SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SECUENCE CHARACTERISTICS:

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US-08-845-258-45
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/08845258 patent No. 6183976
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ITP: 98104

ITP: 98104

ITP: 98104

ITP: 98104

ITP: 98104

ITP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floopy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/845,258

APPLICATION NUMBER: US/08/845,258

APPLICATION APP-1997

FILING DATE: 24-APF-1997

FILING DATE: 24-APF-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 53

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
ADDRESSEE: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Seattle
                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J. 31,392
REGISTRATION NUMBER: 210121.426C1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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24-APR-1997
N: 435
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pred. No. 4.3e-07;
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Length 4223; Indels

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Result
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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    2967
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35828
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3791
294
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5000
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                   US-08-820-170A-38
US-09-273-565-38
US-09-273-565-38
US-09-565-58-38
US-09-565-59-39
US-09-565-58-39
US-09-661-468-39
US-09-661-468-39
US-09-661-468-39
US-09-667-773B-28
US-09-449-218D-17
US-08-675-773B-3
US-08-675-773B-3
US-08-545-196B-15
US-09-399-913-39
US-09-399-913-39
US-09-399-913-39
US-09-534-638-6
US-09-399-913-39
US-09-534-638-7
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                                       Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 26, Appl Sequence 27, Appl Sequence 17, Appl Sequence 3, Appl Sequence 3, Appl Sequence 4, Appli Sequence 4, Appli Sequence 15, Appl Sequence 39, Appl Sequence 39, Appl Sequence 31, Appl Sequence 31, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, A
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Sequence
Sequence
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                                                                                                                                                               Best Local Similarity Matches 135; Conserv
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Best Local
                                                             1312 TGTGAAGACATGAGTGTGGTGCTGAAGGGCGCCATTACTGTCGTGAAAATACAATGTGT 1371
                 978 GTGAACACCCCGGGCTCGTTTAAGTGCTCCTGTCAGGATGGTTTTCGTCTGACGCCTGAG 1037
                                                                                                            918 TGTGAGGACATGGATGAGTGTGCTACCCCATGGACTCACAACTGCTCCAACAGCAGCTGT 977
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29 45.8 3.4 1851 4 US-09-135-080-5 30 45.8 3.4 3740 4 US-09-135-080-5 31 45.6 3.4 3740 4 US-09-162-274A-6 31 45.6 3.4 3925 4 US-08-793-044-1 32 45.4 3.4 155 1 US-08-222-177A-19 33 45.4 3.4 3854 2 US-08-720-484A-1 34 45.4 3.4 3854 4 US-09-398-239-1 35 45.4 3.4 3854 4 US-09-398-239-1 36 45.2 3.4 3854 4 US-09-398-239-1 37 45 3.3 622 4 US-08-222-177A-36 37 45 3.3 2710 1 US-08-487-748A-8 39 45 3.3 2710 1 US-08-480-070C-8 40 45 3.3 2710 4 US-08-89-583A-8 41 45 3.3 2710 4 US-08-69-583A-8 42 45 3.3 2710 4 US-08-937-399-8 43 3.3 2710 4 US-08-937-399-8 44 45 3.3 2710 4 US-09-313-357-8 45 3.3 2710 4 US-09-313-337-8 45 3.3 2710 4 US-09-313-337-8
. 8 3.4 1851 4 US . 6 3.4 3925 4 US . 6 3.4 3925 1 US . 4 3.4 3854 2 US . 4 3.4 3854 4 US . 5 3.3 2710 1 US . 5 3.3 2710 4 US . 6 3.3 2710 4 US . 7 3.3 2710 4 US
4 4 US 4 1 US 1 US 2 US 3 US 4 US 3 US 4 US 4 US 4 US 4 US 8 US 8 US 9 US 9 US 9 US 9 US 9 US 9 US 9 US 9
SSD
US-09-135-080-5 US-09-162-274A-6 US-08-793-044-1 US-08-222-177A-19 US-08-222-177A-19 US-08-38-239-1 US-08-38-239-1 US-08-222-177A-36 US-08-487-748A-8 US-08-487-748A-8 US-08-487-748A-8 US-08-829-525-8 US-08-829-525-8 US-08-829-525-8 US-08-829-535-8 US-08-837-399-8 US-08-337-399-8 US-09-313-337-8 US-09-313-337-8 US-09-333-337-8 US-09-333-337-8

ALIGNMENTS

## US-08-820-170A-38 RESULT 1 US-08-820-170A-38 Patent No. 5831058 GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Tsutomu, FUJIWARA APPLICANT: Tsutomu, FUJIWARA APPLICANT: Masato, HORIE APPLICANT: Toyomasa, KATAGIRJ Sequence TELEX: 6491103 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 293-7060 TELEFAX: (202) 293-7860 TOPOLOGY: linear MOLECULE TYPE: DNA(genomic) CURRENT APPLICATION DATA: APPLICATION NUMBER: US COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS: APPLICANT: TOYOMASA, KATAGIRI TITLE OF INVENTION: HUMAN GENE LENGTH: 2448 k TYPE: nucleic STRANDEDNESS: NUMBER OF SEQUENCES: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CLASSIFICATION: COUNTRY: United States ZIP: 20037-3202 STREET: 2100 Peni CITY: Washington STATE: D.C. FILING DATE: ADDRESSEE: 38, AL NO. 5831058 1: 2448 base pairs nucleic acid Application US/08820170A E: Sughrue, Mion, Zinn, Macpea 2100 Pennsylvania Avenue, N.W single 4.3%; US/08/820,170A 38 Score 57.8; DB 2; Pred. No. 4.6e-08; 0; Mismatches 107; Zinn, Macpeak & Seas #1.30 Length 2448;

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA(genomic)
US-09-055-699-38
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Best Local Similarity
Matches 135; Conserv
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TELEX: 6491103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,699
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1432 TATTCATGTACAGAACATGATGAGTGTATCACAAATCAGCAC---AACTGTGATGAAAAT 1488
                                1038 CTGAGCTGCACTGATGTGGATGAGTGCTCAGAGCAGGGGCTCAGTAACTGTCATGCCCTG 1097
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APPLICATION NUMBER:
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LE OF INVENTION:
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                                                                      20037-3202
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                                                                                                                                                                                                                       Conservative
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Takeshi, WATANABE
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Pred. No. 4.6e-08;
0; Mismatches 107;
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EARLIER FILING DATE: 1998-04-07
EARLIER APPLICATION NUMBER: 08/820,170
EARLIER APPLICATION NUMBER: J8/8210/1996
EARLIER APPLICATION NUMBER: JF 63410/1996
EARLIER FILING DATE: 1996-03-19
EARLIER APPLICATION NUMBER: JF 69163/1997
EARLIER FILING DATE: 1997-03-05
GENERAL INFORMATION:
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING
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SEQ ID NO 38
LENGTH: 2448
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                                                                                                   Sequence 38, Application US/09565538 Patent No. 6333404
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Best Local Similarity
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APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING EN
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CURRENT APPLICATION NUMBER: US/09/273,565A
CURRENT FILING DATE: 1999-03-22
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ORGANISM: Homo sapiens
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55.1%;
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Pred. No. 4.6e-08;
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FILE NEFEKENCE: U-3339
FILE NEFEKENCE: U-3339
CURRENT APPLICATION NUMBER: U5/09/565,538
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 09/273,565
PRIOR APPLICATION NUMBER: 09/05-5,699
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR FILING DATE: 1997-03-05
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ORGANISM: Homo sapiens
US-09-565-538-38
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FILE REFERENCE: Q-53
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Matches 135; Conserv
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SOFTWARE: patentin Ver. 2.1
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US-09-661-468-38
                                            CURRENT APPLICATION NUMBER: US/09/661,468
CURRENT FILING DATE: 2000-09-13
CURRENT FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR PELLING DATE: 1998-04-0-07
PRIOR PELLING DATE: 1997-03-19
PRIOR PELLING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: UP 63410/1996
PRIOR PELLING DATE: 1996-03-19
PRIOR APPLICATION NUMBER: UP 69163/1997
PRIOR APPLICATION NUMBER: UP 69163/1997
PRIOR PELLING DATE: 1997-03-05
                                                                                                                                                                                                                                                                             GENERAL INFORMATION: TSUTOMU
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORLE, WASATO
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
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10 ID NO 38
LENGTH: 2448
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Conservative
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-53599
                                          SEQ ID NOS: 95
PatentIn Ver. 2.1
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pred. No. 4.6e-08;
pred. No. 4.107; Indels
0; Mismatches 107; Indels
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ORGANISM: Homo sapiens
US-09-661-468-38
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Best Local Similarity
Matches 135; Conserv
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US-08-820-170A-39
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GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPRONE: (202) 293-7060
TELEPRONE: (202) 293-7860
TELEPRA: (202) 293-7860
TELEX: 6491103
TELEX: 6491103 IN NO: 39:
INFORMATION FOR SEQ ID NO: 39:
INFORMATIO CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGUENCE CHARACTERISTICS:
LENGUENCE CHARACTERISTICS:
LENGUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTIC
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APPLICANT: Takeshi, WATANABE
APPLICANT: MASSATO, HORIE
APPLICANT: MASSATO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,170A
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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ZIP: 20037-3202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                            MOLECULE TYPE: UP
                                     IMMEDIATE SOURCE:
LIBRARY: Human fetal brain cDNA library
CLONE: GEN-093E05
                                                                                                                                                            HYPOTHETICAL:
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                    TOPOLOGY:
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5831058
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2100 Pennsylvania Avenue, N.W.
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LOCATION: 97..2544
US-08-820-170A-39
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Query Match
Best Local Similarity 55.1%;
Matches 135; Conservative
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US-09-055-699-39
Sequence 39, Applicatic 6005088
Patent NO. 6005088
Patent INFORMATION:
GENERAL INFORMATION:
APPLICANT: Takeshi
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TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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APPLICANT: MASATO, HORIE
APPT TOYME
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CORERIT APPLICATION DATA:

CORRERAT APPLICATION DATA:
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                                                                                     INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 3198 base pairs
LENGTH: 3198 base pairs
                                                                                                                                                                           PRIOR APPLICATION DATA: 08/820,170 APPLICATION NUMBER: 08/820,170 FILING DATE:
                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7860
TELEFAX: (202) 293-7860
TELEX: 6491103
                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                          APPLICATION NUMBER:
                               MOLECULE TYPE:
INMAEDIATE SOURCE:
ITBRARY Human fetal brain cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9, Application US/09055699
6005088
                                                                    STRANDEDNESS:
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20037-3202
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                                                                                nucleic acid
                                                          ESS: single
linear
                                  s: DNA(genomic)
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pred. No. 5.3e-08;
pred. No. 5.3e-107;
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FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
100-055-699-39
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Best Local Similarity 55.3
Matches 135; Conservative
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US-09-273-565-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/273,565A
CURRENT FILING DATE: 1999-03-22
CURRENT FILING DATE: 1998-04-07
EARLIER APPLICATION NUMBER: 08/820,170
EARLIER FILING DATE: 1997-03-19
EARLIER APPLICATION NUMBER: UF 63410/1996
EARLIER APPLICATION NUMBER: UF 63410/1996
EARLIER APPLICATION NUMBER: UF 63410/1997
EARLIER FILING DATE: 1996-03-19
EARLIER FILING DATE: 1997-03-05
EARLIER FILING DATE: 1997-03-05
EARLIER FILING DATE: 1997-03-05
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APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC
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                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (97)..(2544)
US-09-273-565-39
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Query Match
Best Local Similarity 55.1%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                      978 GTGAACACCCCGGGCTCGTTTAAGTGCTCCTGTCAGGATGGTTTTCGTCTGACGCCTGAG 1037
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                                                                                                                                                                                                                                              Score 57.8; DB 4;
pred. No. 5.3e-08;
pred. No. 5.3e-107;
0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                    Length 3198;
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1528 TATTCATGTACAGAACATGATGAGGGTGTATCACAAATCAGCAC---AACTGTGATGAAAAAT 1584

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APPLICANT: HUMLE, MADATU
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: Q-53599
FILE REFERENCE: Q-53599
FILE REFERENCE: Q-53599
CURRENT PILING DATE: 2000-05-05
CURRENT FILING DATE: 1999-03-72
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1996-03-19
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US-09-565-538-39
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LOCATION: (97)...(2544)
US-09-565-538-39
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NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin ver. 2.1
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Best Local Similarity 55.1%;
Matches 135; Conservative
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δõ
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                                                                                                                                                                                                      1038 CTGAGCTGCACTGATGTGGATGAGTGCTCAGAGGGGGCTCAGTAACTGTCATGCCCTG 1097
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                                                                                       1528 TATTCATGTACAGAACATGATGAGTGTATCACAAATCAGCAC---AACTGTGATGAAAAT 1584
                                                          1098 GCCACCTGTGTCAACACAGAGAAGGCGACTACTTGTGCGTGTGTCCCGAGGGCTTTACAGGG 1157
      1158 GATGG 1162
                                                                                                                                              3198
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                                    0; Mismatches 107;
                                                                                                                                                                                                                                                                                         Score 57.8; DB 4;
pred. No. 5.3e-08;
                                                                                                                                                                                                                                                                                                                 Length 3198;
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1645 AATGG 1649

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RESULT 10
US-09-661-468-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: (97)...(2544)
US-09-661-468-39
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APPLICANT: WATANABE,
APPLICANT: HORIE, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1996-03-19
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR APPLICATION NUMBER: 1997-03-05
PRIOR FILING DATE: 1997-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: Q-53599
FILE REFERENCE: Q-53599
CURRENT APPLICATION NUMBER: US/09/661,468
CURRENT FILING DATE: 2000-09-13
CURRENT FILING DATE: 2000-09-13
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PRIOR FILING DATE: 1998-04-07

PRIOR APPLICATION NUMBER: 08/820,170

PRIOR APPLICATION NUMBER: 08/820,170

PRIOR FILING DATE: 1997-03-19

PRIOR FILING DATE: 1997-03-19
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Query Match
Best Local Similarity 55.1%;
Hatches 135; Conservative
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                                                                                  Sequence 26, Application US/08637823B

Patent No. 6184031

Patent INFORMATION: Philippe
APPLICANT: Skamene, Emil
PAPPLICANT: S
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 US-08-637-823B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1408 TGTGAAGACATCGATGAGTGTGTGCTGAAGGGCGCCATTACTGTGTGAAAATACAATGTGT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1468 GTCAACACCCCGGGTTCTTTATGTGCATCTGCAAAACTGGATACATCAGAATTGATGAT 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     918 TGTGAGGACATGGATGAGTGTGCTACCCCATGGACTCACAACTGCTCCAACAGCAGCTGT 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1098 GCCACCTGTGTCAACACAGAAGGCGACTACTTGTGCGTGTGTGCCCGAGGGCTTTACAGGG 1157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              978 GTGAACACCCGGGCTCGTTTAAGTGCTCCTGTCAGGATGGTTTTCGTCTGACGCCTGAG 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1645 AATGG 1649
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                                                    STREET:
                                                                            ADDRESSEE:
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                       Hackensack
New Jersey
                                                           411 Hackensack Ave
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                                                                                                                                                                                  DNA SEQUENCES THAT ENCODE A NATURAL RESISTANCE TO INFECTION WITH INTRACELLULAR PARASITES
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pred. No. 5.3e-08;
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

ZIP: 07601

MEDIUM TYPE:

READABLE FORM: TYPE: Floppy disk

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                                                                                                                                                                                                                                                        US-08-907-706-2
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                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                               tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                          2237 CCTGCCTGCTTCTGCGTGGGGGCCACGGGTTGGCATCAGGTGTCTCCAGTCTCTACCA 2296
                                                                STREET: 31.
                                                                                                                   NUMBER OF SEQUENCES: 8
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ORIGINAL SOURCE: Mus musculus
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LENGTH: 2967 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 65.8%; les 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 50.
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COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson, David A.
REGISTRATION NUMBER: 26,742
                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                       3 CCTGGATGCTGGTAATGATGGTAACCTCCTGGTTCACTCTGGCTGAAGCCAGTAACT 62
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                                                                                                                                                                                                               INFORMATION:
                                                             CA
                                                                                                                                               INVENTION:
                                                                                                                                                                                                                             Application US/08907706
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                                                                                         3174 Porter Dr
                                                   USA
                                                                                                                                                                     Hillman, Jennifer L. Guegler, Karl J.
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                                                                                                                                                         Shah, Purvi
                                                                                                                                                                                                   Bandman, Olga
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IBM Compatible
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                                                                                                     Incyte Pharmaceuticals, Inc.
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                                                                                                                                              NADH DEHYDROGENASE SUBUNITS
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Pred. No. 4.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
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23 ATGGTAACCTCCTGGTTCACTCTGGCTGAAGCCAGTAACTCAACAGAAGCGAGTAAGTGT

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; NAME/KEY: misc_feature
; LOCATION: (1)...(35828)
; OTHER INFORMATION: n = A,T,C or G
US-09-449-218D-17
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Best Local Similarity
"~+ches 65; Conserve
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                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 17
   Matches
                                                     Query Match
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                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
TITLE OF THE COMPOSITION COMPOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/449, 218D CURRENT FILING DATE: 1999-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                              ENGTH:
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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es 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                 35828
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Van Ness, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mulligan, John T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kovacevich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1560 base pairs
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            ID NOS:
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FastSEQ for Windows Version
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73.0%;
                               66.3%;
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Score 48; DB Pred. No. 0.00 0; Mismatches
      0;
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Pred. No. 6.8e
0; Mismatches
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                                                              DB 4;
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5.8e-06;
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PRIOR PRILIGE DATE: 1999-02-19
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR NUMBER: SWEDEN 9703914-2
PRIOR PRILING DATE: 1998-10-27
PRIOR PILLING DATE: 1997-10-27
PRIOR PILLING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
PRIOR PILLING DATE: 1998-03-16
PRIOR FILLING DATE: 1998-03-16
PRIOR FILING DATE: NUMBER: SWEDEN 98008775-2
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GENERAL INFORMATION:
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Sequence 60, APP-
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CURRENT APPLICATION NUMBER: US/09/422,936
CURRENT FILING DATE: 1999-10-22
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PRIOR FILING DATE: 1998-07-17
PRIOR FILING DATE: 1998-07-17
UNMBER OF SEQ ID NOS: 850FTWARE: Fastseq for Windows Version 4.0
SOFTWARE: Fastseq for Windows Version 4.0
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SEQ ID NO 60
LENGTH: 15652
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ITLE OF INVENTION: 1
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NAME/KEY: misc_feature
LOCATION: (1)...(15652
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OTHER INFORMATION: k = G or T/,
OTHER INFORMATION: b = G, C, O
OTHER INFORMATION: h = A, C, O
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LOCATION: (1)...(15652)
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OTHER INFORMATION: n A,
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LOCATION: (3419)...(3444)
NAME/KEY: intron
LOCATION: (3445)...(3908)
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(12407)...(12820)
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1998-07-17
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A, G, or C
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Query Match
Best Local Similarity 63.5%;
Matches 73; Conservative
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US-08-675-773B-3/C
                                                                                                                                      UPERMITING SISTEM: FRIENCE #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSENT APPLICATION NOBER: US/08/675,773B
APPLICATION NOBER: US/08/675,773B
APPLICATION NOBER: US/08/675,773B
APPLICATION NOF PARATION:
APPLICATION THE P. 28,005
REGISTRATION NUMBER: 28,005
TELEPRONE: 202-628-519
TELEPRONE: 202-638-519
TELEPRONE: 202-737-3528
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patent No. 6166288
patent INFORMATION:
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15195)...(15652)
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CADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 SEVENTH STREET, N.W., SUITE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHARMA. AJAY
APPLICANT: SHARMA. METHOD OF PRODUCING TRANSGENIC ANIMALS
TITLE OF INVENTION: FOR XENOTRANSPLANTATION.
TITLE OF INVENTION: FOR XENOTRANSPLANTATION.

NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPACTIONS
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 412 CONTRECTOR WASHINGTON CITY: WASHINGTON CTATE: D.C.
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                                                   TOPOLOGY: 11
MOLECULE TYPE:
8-675-773B-3
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LOGAN, JOHN S
BYRNE, GUERARD W
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Pred. No. 0.00018;
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Perfect score:
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BF783842 602109765
BI100241 602885296
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BF785672 602112079
BF783809 602109729
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784752 602111	46618 ul01d06.v	781608 6021043	687200 60210222	746802 ul07f03.v	786646 6021114	563313 uk27d08.y	[100595 60288674	533234 60207388	786238 60211264	v106846 um34c09.	789452 6021035	788214 60211344	788084 60211329	786518 60211075	780526 60210406	786743 60211191	987598 ul86c05.y	103612 60288876	1101569 60288737	788589 60211446	BI100943 602886267	787946 60211313	789723 60210375	F783802 60210972	BF687119 60210292	747396 uloshos	1747914 ulo3h09 v	3970639 60283851	F781466 602107	F786633 60210858	F785008 60211095	986595 uč81a10	527894 uj30dll.v	W211279 u129h0	527836 u129q04.v	F789128 602104	G969349 60283683	G972563 60284114

## ALIGNMENTS

KEYWORDS SOURCE ORGANISM FEATURES RESULT 1 BF783842 COMMENT REFERENCE DEFINITION VERSION ACCESSION AUTHORS TITLE JOURNAL In Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM9848 row: b column: 17
High quality sequence stop: 654.
Location/Qualifiers house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 656)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC) BF783842 656 bp mRNA linear EST 12-JAN-2001 602109765F1 NCI\_CGAP\_Kid14 Mus musculus cDNA cione IMAGE:4237744 5', mRNA sequence.
BF783842 EST. BF783842.1 GI:12088878 рe

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Query Match
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SOURCE
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DEFINITION
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AUTHORS
            TITLE
JOURNAL
COMMENT
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602885296F1 NCI_CGAP_Kid14 Mus musculus
5', mRNA sequence.
51,00241
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/organism_"FVB/N"
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/note="Drign: kidney; Vector: pCMV-SPORT6; Site_1: Oligo dT.
/note="Drign: Kidney; Vector: pCMV-SPORT6; Site_1: Oligo dT.
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NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email cgapbs-remail nih.gov
                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 703)
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pred. No. 5.4e-146;
p; Mismatches 3;
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Sciurognathi; Muridae; Murinae; Mus
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CDNA Clone IMAGE:5040646
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602103506F1 NCI_CGAP_Kid14 Mus m
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/strain="FVB/N"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
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CDNA Clone IMAGE:4221817
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prissue procurement: Jeffrey E. Green, M.D.
Tissue procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
CDNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
Clone distribution: MGC clone distribution information can
Clone distribution: M.A.G.E. Consortium/LINL at:
found through the I.M.A.G.E. Consortium/LINL at:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone=lib="NICI_CGAP_Kid14"
/clone=lib="Nici" Note: this is a NCI_CGAP_Library. | "
Technologies Note: this is a NCI_CGAP_Librar
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pred. No. 5.8e-146;
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5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 1087)

1 (bases 1 to 1087)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Fissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Incyte Genomics Inc.

DNA sequencing by: Incyte Genomics Inc.

Clone distribution: MGC clone distribution information can

Clone distribution: MGC clone Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. 691.

http://image.llnl.gov

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Contact: Robert Strausberg, Ph.D.
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pred. No. 6.5e-146;
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musculus cDNA clone IMAGE:4240339
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 GTGCTCCTGTCAGGATGGTTTTCGTCTGACGCCTGAGCTGAGCTGCACTGATGTGGATGA
                                  GTGCTCCTGTCAGGATGGTTTTCGTCTGACGCCTGAGCTGAGCTGCACTGATGTGGATGA 1060
                                                                     TACCCCATGGACTCACAACTGCTCCAACAGCAGCTGTGTGAACACCCCGGGCTCGTTTAA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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quality sequence stop: 670.
Location/Qualifiers
                                                                                                                                                                                                                                                                                    Conservative
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/db_xref="taxon:10090"
/clone="IMAGE:4237926"
/clone="INFOICCGAP_Kid14"
/clone="DHCIGGAP_Kid14"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
/site_2: SalI; Cloned unidirectionally. Primer: Oli
Site_2: SalI; Cloned unidirectionally. Primer: Oli
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 244 c 290 g 201 t 1 others
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/strain≈"FVB/N"
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                                                                                                      Local Similarity 99.7 tes 528; Conservative
                                  GCAGGACGGTGTTCTGAATGCCACAACCACGCCACCTGCACGGTGGATGGTGGTCACA 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LLAM10956 row: i column: High quality sequence stop: 768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 801)
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                                                                                                                                                                                             165
                                                                                                                                                                                    /organism="Mus musculus"
/strain="FVB/N"
/strain="FVB/N"
/db_xref="taxon:10090"
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/note="Organ: kidney: Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: kidney: Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
65 a 209 c 246 g 181 t
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Pred. No. 1.1e-142;
D; Mismatches 3;
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musculus
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602841149F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4975380
5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LINI)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (CLNI)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Clone distribution information can
Clone distribution: MGC clone distribution
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High quality sequence stop: 705.
High quality sequence stop: 705.
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                  161
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/clone="normal" with the constructed by Life average insert size 1.75 kb. Constructed by Life average insert size in a NCI_CGAP Library. | "Technologies. Note: this is a NCI_CGAP Library. | "Technologies." | "Technologies. Note: this is a NCI_CGAP Library. | "Technologies. Note: this is a NCI_CGAP Library. | "Technologies." | "Tech
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BG969349
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Enkaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae; Mus
RS NHH-MGC http://mgc.nci.nih.gov/.
RS NHH-MGC http://mgc.nci.nih.gov/.
Enail: Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AL Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cyapbs-remail.nih.gov
Email: cy
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602836830F1 NCI_CGAP_K1d14 Mus musculus
5', mRNA sequence:
BG969349
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                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov k column: 08 plate: LLAM10956 row: k column: 08
                                                    quality sequence stop:
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/organism="Mus musculus"
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pred. No. 1.1e-142;
pred. Mismatches 3;
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Sciurognathi; Muridae; Murinae; Mus
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CDNA clone IMAGE:4971391
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BF789128
                                                                    REFERENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
E 1 (bases 1 to 964)
E NIH-MGC http://mgc.nci.nih.gov/.
S National Institutes of Health, Mammalian Gene Collection
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
L Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Emmali: ogapbs-remail.nih.gov
Emmali: ogapbs-remail.nih.gov
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                            5', mRNA sequence.
BF789128
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602104981F1 NCI_CGAP_Kid14 Mus
5', mRNA Securer
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/db_xref="taxon:10090"
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/clone_tib="NCI_TONE"
/note="0rgan: kidney; Vector: pcMV-SPORT6; Site_1: Not /note="0rgan: kidney; Vector: pcMV-SPORT6; Site_1: Note-indiality primer: Oligo /note="0rgan: kidney; Vector: pcMV-SPORT6; Site_1: Note-indiality pcm, N
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cDNA clone IMAGE:4222772
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816 GCAGGACGGTGTTCTGAATGCCACAACCACGCCACCTGCACGGTGGATGGTGTGGTCACA 875
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Clone distribution: MGC clone distribution information can Clone distribution: MGC clone of through the I.M.A.G.E. Consortium/LLNL at: found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov b column: 21 plate: LLAM9810 row: b column: 21 plate: LLAM9810 row: 697.

High quality sequence stop: 697.

Location/Qualifiers
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                                                        AI527836.1
house mouse
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/db_xref="IMAGB:4222772"
/clone=_lib="NCI CGAP_Kid14"
/clone_lib="NCI CGAP_Kid14"
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/clone_lib="NCI CGAP_Kid14"
/clone="NCI CGAP Library: Vector: pcWV-SPORT6; Site_1: /note" norgan: kidney; Vector: pcWV-SPORT6; Site_1: Cloned unidirectionally. Primer: Oli /note="norgan: kidney; Vector: pcWV-SPORT6; Library: libr
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/strain="FVB/N"
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pred. No. 1.2e-142;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 564)
1 (bases 1 to 564); Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Persor
Underwood, K., Steptoe, M., Theising, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R.,
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R.,
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R.,
B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
Waterston, R. and Wilson, R.
1055
                                                                                                                                                                                                                                                          132 TeTeCTACCCCATGGACTCACAACTGCTCCAACAGCAGCTGTGTGAACACCCCCGGGCTC 191
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Contact: Marra M/Washu-NCI Mouse EST Project 1999
Contact: Marra M/Washu-NCI of Medicine
Washington University School of Medicine
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This clone is available royalty free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
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Fax: 314 286 1810
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                                                   primer: custom primer used h quality sequence stop: 318.
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/lab_host="pullo"
/lab_host="p
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/db_xref="taxon:10090"
/clone="IMAGE:1921398"
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/sex="female"
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Pred. No. 3e-142;
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Mammalia; Eutheria;
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Other ESTs: ul29h09 x1
Other ESTs: ul29h09 x1
Contact: Maira M/WashU-NCI Mouse EST project 1999
Contact: Maira Mills Mouse EST project 1999
Contact: Maira Mills Mouse EST project 1999
Contact: Maira Mills Mouse EST project 1999
Contact: Maira M/WashU-NCI M/WashU-NCI Mouse EST project 1999
Contact: Maira M/WashU-NCI M/W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
TMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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h quality sequence stop: 37,
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GI:6517227
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/sex="female"
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/clone="IMAGE:2099777"
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1176 TGCTCCCCAGGCTCCTGTGAGCCAGGACTGGACTGCTTGCCCCAGGGCCCGGATGGAAAG 431
372 TGCTCCCCAGGCTCCTGTGAGCCAGGACTGGACTGCTTGCCCCAGGGCCCGGATGGAAAG 431
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                                                                                                        Unpublished (1999)
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST project 1999
Contact: Marra Markay, Box 8501, St. Louis, MO 63108, 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, 4444 Forest Park
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/db_xref="taxon:10090"
/clone="IMAGE:1921461"
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/sex="female"
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pred. No. 5.7;
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                                          TGTGCTACCCCATGGACTCACAACTGCTCCAACAGCAGCTGTGTGTAACACCCCGGGCTCG 995
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 713)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashIngton University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uc81g10.y1 Sugano mouse kidney mkia Mus musculus IMAGE:1432098 5' similar to gb:M15881 UROMODULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: primer name ambiguous High quality sequence stop: 349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                  [ATGTGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraiII adaptor [TGTTGGCCTACTGG] digested and cloned into distinct DraiII sites of the pME185-FL3 vector [5' site CACTGTGTG, 3' site CACCATGTG]. XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments (1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: kidney; Vector: pME18S-FL3; Site_1: Di
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand
was primed with an oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL"
/db_xref="taxon:10090"
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/sex="female"
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                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
Plate: LLAM9851 row: d column:
High quality sequence stop: 675.
                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BF785008
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                                                                                    /Clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
1 249 c 314 g 176 t
                                                                                                                                                                                                          /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4238942"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; 1 to 843)

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602108585F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4236788
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188 a 207 c 275 g 172 t 1 others
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nilarity 97.9%;
Conservative
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pred. No. 2.6e-139;
pred. No. 10;
Nismatches 10;
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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SGSS; genome survey sequence.

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ISM retraodon nigroviridis.

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Puteleostei, Neoteleostei, Retraodon nigroviridis

Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei, Neoteleostei, Retraodon nigroviri, Neopterygii; Percomorpha; Tetraodontiformes; Acanthomorpha; Acanthomorpha; Acanthomorpha; Petraodon.

Tetraodontidae; Tetraodon.

Tetraodontidae; Tetraodon.

Tetraodontidae; Tetraodon.

Brottier,P., Guneau,L., Fisher,C., Wincker,P., Brottier,P., Quetier,F.,

E Roses 1 to 394)

Tetraodon nigroviridis DNA sequence

Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J., Weissenbach, J.
                                                          Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis unpublished
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AZ438500 1M0292L05
BH003363 ef27910 x
BH003363 ef27910 x
BH003363 repc1-24-2
BH033951 RPC1-24-9
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ALJO67347 Drosophil
ALJO60767 Drosophil
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ALJO60767 PROGENS-1
AZ653521 RPC1-23-1
AZ658202 fc20a08.9
AZ101052 RPC1-23-4
AZ101052 RPC1-23-4
AZ101052 RPC1-23-4
AZ101331 Tetraodon
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AQ99992 RPCI-23-3
AQ999935 RPCI-23-4
AZ96390 RPCI-23-4
AZ96390 RPCI-23-6
AZ9646118 1M0512C02
AZ9646118 1M0512C02
AZ96064 BB620864
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AZ295388 RPCI-23-2
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AZ295384 RPCI-23-1
AZ896443 RPCI-23-1
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AZ965544 AM0230P04
AZ403008 1M0170P05
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                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 415)
Marra, M., Hillter, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., E., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., F., E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                            Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                               vv83c11.y1 Stratagene mouse skin IMAGE:1229012 5', mRNA sequence. AI466217
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                             Unpublished (1999)
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mouseest@watson.wustl.edu
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/db_xref="taxon:99883"
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/clone=11b="Genoscope sequence ID : C0BG097AH09LP1-end : '/note="Genoscope sequence ID to others
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139; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vv83c11.r1 Stratagene mouse skin
IMAGE:1229012 5', mRNA sequence.
AA762356
AA762356.1 GI:2812103
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                         1 (bases 1 to 452)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                      The WashU-HHMI Mouse
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/note="organ: skin; Vector: Bbluescript SK-; Site_1:
/note="organ: skin; Vector: Bbluescript SK-; Site_1:
/note="organ: skin; Vector: Bbluescript SK-; Site_1:
/note="organ: skin; Vector: Bbluescript Skin from 11 week old C57BL/6 female mice."
/note=skin from 11 week old C57BL/6 female mice.
/note=skin from 12 week old C57BL/6 female mice.
/note="organ: bbluescript" Site_1:
/note="organ: bbluescript" Site_1:
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/db_xref="taxon:10090"
/clone="IMAGE:1229012"
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Fax: 314 286 1810
Email: mouseest@wa
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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A2853376 A2853376 DNA DISCULUS GENOMIC
2M0156105R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UGC2M0156105 K, DNA sequence.
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus. Romandalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Ramandalia; Lo 627)

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Unpublished (2000) Weiss Contact: Robert B. Weiss University of Utah Genome Center
                                                                                                   plasmid inserts
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/strain="c57BL/6"
/db_xref="taxon:10090"
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Pred. No. 9.5e-08;
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AZ974581/c
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ORGANISM
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                                      REFERENCE
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Tel: 801 585 7177

Fax: 801 585 7177

Email: ddunndgenetics.utah.edu

Email: ddunndgenetics.otah.col

Email: ddundgenetics.otah.col

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1783 GGCAGCCTAAGTTGGTCTTGAACTCACTATGAAGCTAGCAATGAGCTTGAGCTTCTGATC 1842
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: plasmid ends
High quality sequence stop: 627
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/lab_host="E: Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="Sex="MD42nv; Purified genomic DNA from M.
/laboratory Mouse DNA Resources/documents/dnares/). The DNA
muscullus C57BL/6J (male) was obtained from the Jackson
/laboratory Mouse DNA Resources/documents/dnares/). The DNA
muscullus C57BL/6J (male) was obtained passage through a
(http://www.jax.org/resources/documents/dnares/). The DNA
/laboratory Mouse DNA Resources/documents/dnares/). The Sheared DNA
was hydrodynamically sheared by repeated passage through a
(http://www.jax.org/resources/documents/dnares/ and T4
0.005 inch orifice at constant velocity. The sheared bNA
was blunt end-repaired with T4 bn polymerase and T4
vas blunt end-right molar excess The 5
polymuclootide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess The 5
electrophoresis vector DNA was prepared from a derivative
electrophoresis vector DNA was prepared from a derivative
of phapa (gil4732114) ghar12972.1), a copy-number
electrophoresis vector DNA was prepared the daptors and
inducible derivative of plasmid R1. The vector was ligated
of purified. The sheared, adaptored mouse DNA was annealed to
with adaptors complementary to the insert adaptors and
of purified. The sheared, and transformed into
purified vector DNA, and transformed into
adaptored vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampiciliin resistance."
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2M0249B14F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0249B14 F, DNA sequence.
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomı, muridae; Murinae; 
                                                                                                                                                                                                                                                                                                                                                              AZ974581.1 GI:13845808
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/organism="C57BL/6J"
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/db_xref="raxon:10090"
/db_xref="nugc2M0156105"
/clone="UUGC2M0156105"
     Dunn, D., Aoyagi, A.,
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.7%;
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Pred. No. 1.1e-07;
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                                                                                                                                                                                                                                                                                                                                     1613 CGCATGCACACACACACACACAAACTGCAAAAGTGAATAAAAAGATATTTCTCACTT 1672
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                                                                             1733 G 1733
                                                                                                                                                                                                                                                                          Local Similarity
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Insert Length: 1000 Std Error:
Plate: 0249 row: B column: 14
Plate: 0249 row: CGTTGTAAAACGACGGCCAGT
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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High quality sequence stop: 517
Location/Qualifiers
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                      G 177
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female" coll strain XLLO-Gold, T1-resistant, F."
/lab_host="E. coll strain XLLO-Gold, T1-resistant, F."
/lab_host="E. coll strain XLLO-Gold, T1-resistant, F."
/lab_host="E. coll strain yurified genomic DNA from M.
/note="vector: pwp42nv; purified genomic DNA from the Jackson /note="vector" purified note: purified note: purified passage through a (http://www.jax.org/resources/documents/dnares/). The DNA raboratory Mouse DNA resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orlified with T4 DNA polymerase and T4 0.05 inch orlified and proparative polymerase and T4 0.05 inch orlified not size-selected for a 9.5 to liquated to the blunt ends in high molar excess. The liquated to the blunt ends in high molar excess. The liquated to the blunt ends in high molar excess. The liquated to E. S. kb range using preparative agarose gel adaptored NA was purified and size-selected for a 9.5 to liquated of pwp42 (gil4732114|gb|aF129072.1), a copy-number electrophoresis: vector NA was prepared from a derivative of plasmid R1. The vector was ligated inducible derivative of plasmid R1. The vector was ligated inducible derivative of plasmid R1. The vector was and inducible derivative of plasmid R1. The vector was annealed to purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into and selected for ampicillin resistance."

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milarity 62.4%;
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/db_xref="taxon:10090"
/clone="UUGC2M0249B14"
/clone="UUGC2M0249B14"
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Matches 100; Conserv
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus.

Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Mus.

Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Mus.

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                                                                                                       Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.(
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Plate: 0007 row: F column: 19
Plate: 0007 row: F column: 19
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       199
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Contact: Robert B.
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Fax: 801 585 7177
Laboratory Mouse DNA RESOURCE (Accuments/dnares/). The DNA (http://www.jax.org/resources/documents/dnares). The DNA (http://www.jax.org/resources/documents/dnares) through a (http://www.jax.org/resources/documents/dnares) through a was hydrodynamically sheared by repeated passage through a (0.05 inch orifice at constant velocity. The sheared DNA (0.05 inch orifice at constant velocity. The sheared and size-selected for a 9.5 to ligated to the blunt ends in high molar excess. The polynucleotide kinase. Adaptor oligonucleotides were adaptored DNA was purified and size-selected for a 9.5 to 119ated to the blunt ends in high melar excess. The 10.5 kb range using preparative agarces gel adaptored using preparative agarces gel adaptored as sing preparative agarces for was ligated of pwDA2 (gil4732114|gb)AF129072.1), a copy-number lettrophoresis. Vector DNA was prepared from an inducible derivative of plasmid R1. The vector was and inducible derivative of plasmid R1. The vector was annealed to with adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors and adaptored vector DNA, and transformed into purified. The sheared, adaptored mouse DNA was annealed to chemically-completent E. Looli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone="UUGC1M0007F19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/lab_host="Yector: pwp42nv; Purified genomic DNA from M.
/note="Yector: pwp42nv; Purified genomic DNA from the Jackson musculus C57BL/6J (male) was obtained from the Jackson mu
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pred. No. 3.5e-07;
pred. No. 47;
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AL514757 RNA sequence.
AL514757
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BP 191 91006 EVRY cedex - France
BP 191 seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Email: seqrefégenoscope.cns.fr, Web : Location/Qualifiers
428 TATACACACACACACACACAYAYAYAGCASACACATATATATATATAYAYAYAYATATATATAT
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                                         GATCCTTATATCTACACTCTCAAGTGCCCAGATTATAAGTGTGCACCACTATACTCAGTT 1898
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milarity 44.7%;
Conservative 15
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/ob_xref="taxon:966"
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/db_xref="taxon:966"
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/clone=lib=lib="lib"
/clone=lib=lib="lib"
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pred. No.
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Determination of this BAC-end sequence was carried out as part of a petermination of the Barkeley Drosophila Genome project (BDGP).

Determination of the Barkeley Drosophila Genome project (BDGP).

Collaboration with the Barkeley Drosophila Genome project (BDGP).

The BDGP is constructing a physical map of further information melanogaster genome using these BGCs. For further prosophila melanogaster BGC library was preparable by Kazurtoyo Gooegaat and please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila part of the BDGP from the cancer and the Roswell Park Cancer Institute in Buffalo, melanogaster in pieter de Jong's laboratory in the pepartment of cancer Genetics at the Roswell Park Cancer Institute in BDGP from the Cancer Genetics in amed RogC198 and was constructed by partial NY. The library is named to DNA provided by the BDGP from the BDGP is not be pland EST libraries. A more detailed description of the library or isogenic strain y2; on bw SP, detailed description of the library or pland EST libraries. A more detailed description of the library or and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
Drosophila melanogaster from Drosophila melanogaster (fruit BACR09C16 of RPCI-98 library from Drosophila melanogaster (fruit 1), genomic survey sequence.
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Brosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Bukaryota; Medopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Drosophila.
Ephydroidea; Drosophilidae; Drosophila.
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ATAAATGGAGAGGGGGTCAAAGATGGAGCAAAGGAAGGATGAGCAAGAAAATGGTGGAT 557
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/note="end: TET3"
/note="end: TET3"
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pred. No. 1.8e-06;
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Contact: Robert B. Weiss

Contact: Robert B. Weiss

University of Utah

University of Utah

University of Utah
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Fax: 801 585 7177
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/lab_host="E. Coli strain XIIO-Gold, Ti-resistant, F-"
/lab_host="E. Coli strain XIIO-Gold, Ti-resistant, F-"
/lab_host="E. Coli strain XIIO-Gold, Ti-resistant, Folk Andrew Vector: PWD42nv; Purified genomic DNA from the Jackson
/note: "Vector: PWD42nv; Purified from the Jackson
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/db_xref="taxon:10090"
/db_xref="tuugc1M0228E10"
/clone="UUGC1M0228E10"
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                                                                                                                                                                                                                                                                                                                                                   Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory Cold Spring Harbor Harbor, NY 11724, USA PO BOX 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884

Fax: 516 367 8874
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Contact: W. Richard McCombie
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113 g 167 t copy-number induced in the purified vector DNA, and transformed into purified vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicilin resistance."
                                                                                                                                                                                                                                                                                                          Email: mccombie@cshl.org
plate: ef27 row: g col
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/clone_lib="TO1000" x reads, p2ero-2 for b and g /clone_lib="TO1000" x reads, p2ero-2 for b and g /note="Wector: M13 for x reads whole genome shotgun reads; Site_l: EcoRv; DNA prepared as whole some plastid reads; Site_l: EcoRv; DNA prepared way contain some plastid reads; From young, green leaves. May contain some plastid reads; DNA provided by Dr. Tom obborn, University of DNAS. DNA provided by Dr. Tom obborn, DNAS DNA provided by Dr. Tom ob Agronomy."
                                                                                                                                    /organism="Brassica oleracea"
/db_xref="taxon:3712"
/clone="ef27910"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 700.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0292 row: L column: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1M0292L05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0292L05 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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801 585 7177
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           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDd2 (gil4732114 lgblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inserts
                                                                                                                                                                                                                        /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg., 20 S.
                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0292L05"
                                                                                                                                                                                                                                                                                                                       /clone_lib--"Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                       /sex="Male"
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                                                                           202
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Contact: Shaying Zhao
Department of Eukaryottic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24.
                                                                                                                                                                                                                                                                                                                                   Plate: 297 row: I column: Seg primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                             library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 297 row: I column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Other_GSSs: RPCI-24-297122.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
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RPCI-24-297122.TV RPCI-24 Mus musculus genomic clone RPCI-24-297122
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a 120 c 106 g 219 t 2 others
                                                                  /Gell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
1 to 618)
                                                                                                                                                                         /db_xref="taxon:10090"
/clone="RPCI-24-297122"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                            location/Qualifiers
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3e-06;
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3.3%;

Score 67; Pred. No.

DB 17; 5.9e-06;

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JOURNAL
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CATGGCCATGTTTTTTTTTTTTATGAAACACACGCACAGGCACAGGCACTCACGTGTGCGC 1575
                                                                                                                          99;
                                                                                                                                                                                                                                                                                                                         Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weissenbach, J.

Charaterization and repeat analysis of the compact freeheater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL192598.1 GI:7830702
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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Roest-Crollius, H., Jaillon, O., Dasilva, C.,
Bouneau, L., Billault, A., Quetier, F., Sauri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bernot, A., Fizames, C., Wincker, P., Saurin, W. and Weissenbach, J. Human gene number estimate provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis genome survey 260J01 of library G from Tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodontidae; Tetraodon 1 (bases 1 to 762)
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                       Similarity
                                                                                                                                                                                                     256
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                                                                                                                          Conservative
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                                                                                                                                                                                           /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="260J01"
/clone="260J01"
/clone_lib="G"
/clone_lib="G"
/note="Genoscope sequence ID : COAG260CE01LP1-end
/note="Genoscope 154 t 19 others
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                     3.3%;
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Pred. No. 6.1e-06;
8; Mismatches 60;
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sequence
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ey sequence T7 end of clone
nigroviridis, genomic survey
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Saurin,W., Bernot,A.
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Neoteleostei;
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of clone
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
TGTGGCAGCCTAAGTTGGTCTTGAACTCACTATGAAGCTAGCAATG-ACCTTGAGCTTCT 1838
                                                            ACACACATATATACNCGCGCGCACACACATATAYACACAYATATAYAYACATACNCAC
                                                                                                   CTATTTTGTACTAGAGGGAGGTTATAAATTATTGTTATTGTTATATTCTATTTTACTGTT
                                                                                                                                                                                     ATATTTCTCACTTTGGCAAAGTGGAAGGTTGATCAAAATGAAAGTTATACTCAGAA 1719
                                                                                                                                                                                                                          ACACACACACACGCATGCACACATGCACCACACACAAACTGCAAAAGTGAATAAAAAG 1659
                                                                                                                                                                                                                                                                                                            210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATATTTCTCACTTTGGCAAAGTGGATGGAAAAGTTGATCAAAATGAAA 1706
                                                                                                                                            ACACACATGTNNATATATACACACACACACACATACACACACACATACACACGTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS007JJ 1203 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR15F04 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope
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Drosophila melanogaster
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/note="end : TET3"
310 c 52 g
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 NNACACATANANANANANNCNCACACACATNNNNNNNTNNACANCGCACACATATACACA 588
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ORIGIN
                                                  Ş
                                                                                                  3.3%;
Query Match 62.7%;
Best Local Similarity 62.7%;
Matches 104; Conservative
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Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
19712 Medical Center Dr., Rockville, MD 20850, USA
19712 Medical Center Dr., Rockville, MD 20850, USA
19712 Medical Center Dr., Rockville, MD 20850, USA
19712 1900
Tel: 301 838 0208
Tel: 302 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           471 bp DNA linear GSS 25-JAN-2001
AZ/29180
RPCI-24-99E21.TJ RPCI-24 Mus musculus genomic clone RPCI-24-99E21,
DNA sequence.
1756 ATTGTTATATTCTATTTTACTGTTTGTGGCAGCCTAAGTTGGTCTTGAACTCACTATGTA 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Chateman C Nringot D Towins Musiculus
Dasses 1 to 471)
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Russell,D., de Jong,P. and Fraser,C.M.
Russell, End Sequences from Library RPCI-24
Rouse BAC End Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Other_GSSs: RPCI-24-99E21.TV
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism."Mus musculus"
/strain.="c578L/6J"
/strain.="taxon:10090"
/db_xref.="taxon:10090"
/clone.=lib="RPCI-24"
/clone.lib="RPCI-24"
                                                                                                                                                                                                                                                                                   /cell_type="Spleen/Brain" Site_1: BamH1; Site_2: BamH1; The /note="Yector: pTARBAC1; Site_1: BamH1 pieter de Jong: The /note="Yector : pTARBAC1; PTARBAC1 cloning vector at the RPCI-24 Mouse BAC Library pTARBAC1 cloning vector at the library was longed in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
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pred. No. 6.3e-06;
pred. No. 6.3e-62;
0; Mismatches 62;
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Search completed: February 17, 2003, 16:06:32 Job time : 2578.96 secs
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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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(without alignments)
12670.391 Million cell updates/sec
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AL066537 Drosophil
AL063921 Drosophil
AL098379 Drosophil
AL098379 Drosophil
AL098595 Drosophil
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
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                                                                                pirect Submission plants of the proscope of the sequences of the submitted (02-JUN-1999) Genoscope of this sequence was carried out as part of the pill submission of this pactor of sequence was carried out as part of the proscophila proscophila genome project (BDGP) occlaboration with the Berkeley Drosophila denomed the proscophila occlaboration with the sequence was referred to proscophila of the proscophila of the proscophila occlaboration with the sequence by sequence was and the please see http://www.fruitfly.org the BDGP Drosophila of the proscophila occlaboration of the proscophila of the proscophila occlaboration of the proscophila of the proscophila occlaboration occlabor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         997 bp DNA linear GSS 03-JUN-199' Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit Ely), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
Drosophila melanogaster.
Drosophila metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Drosophila metazoa; Arthropoda; Brachycera; Muscomorpha;
Eukaryota; Metazoa; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Drosophila.
Ephydroidea; Drosophila.
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AL1062049 Drosophil
AL108811 Drosophil
AL108818 Drosophil
AZ895924 RPCI-24-9
AZ895921637 RPCII1-93
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AL101102 Drosophil
AL105102 Drosophil
BH055477 RPOI 24 3
BH0554972 ZM0220F20
AL108619 Drosophil
AL108815 Drosophil
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AL106237 Drosophil
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BB206913 BB20691.rl
R89145 yp09901.rl
R89145 yp09901.rl
AL106185 Drosophil
AL106185 Drosophil
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AL26596 Drosophil AL065946 Drosophil AL065946 Drosophil AL065946 UT-E-DA1-BE762802 QV3-NT002BE762802 QV3-NT002BE762802 QV3-NT0504 AL163102 yr53e01.r1
AL166732 yr53e01.r1
AL166732 yr53e11.r1
AL166732 yr53e11.r1
AL166732 zo86d08.r
ANB54757 QV0-CT026
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 ATGAGATCCAGTGACAAGCTCATCTCTAGATGTCTGCATACCAATAAGTGACCCATCATT 123
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LOCUS
DEFINITION
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/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone="BACR12K22"
/clone_1ib="RPCI-98"
/note="end : TET3"
/note="end : TET3"
258 t 538 oti
  987 bp
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Drosophila melanogaster genome s
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Pred. No. 1.4e-05;
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3 of BAC #
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr)
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr)
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr)
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr)
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr)
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr)

The BDGP is constructing a bequence was carried out as part of a phetering these BACS. For further information
melanogaster Genome using these BACS. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
melanogaster BAC library de Jong's laboratory in the Department of
melanogaster BAC library de Jong's laboratory in the Departial
Auron Mammoser in pieter de Jong's laboratory in the Departial
Auron Mammoser in pieter of Jong's laboratory in the BDGP from the
Cancer Genetary is named RPOI-98 and was constructed by partial
Auron Mammoser in Dieter of Jong's laboratory from the BDGP from the ST library or
isogenic strain y2; cn bw sp, the same strain used for the library or
isogenic strain y2; cn bw sp, the same strain used for the library
or isogenic strain y2; cn bw sp, the same strain library, or
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fly), genomic survey sequence.
ALD66537
ALD66537.1 GI:4942778
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; muscomorpha;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Drosophila.
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                        435 ANTOCACATATOTAAAGOTATAGAGATAATTTCATGCACTATAGCTTTCAGTACTATCGT 494
                                                                                                                                                                                                                                                                                                                                               748 WICT-CHOCYTCOXYCYYYTTTYTYTYTYTTTTTCCXCYHCYYCYYCYYCYYYYYYTYTCT
                                                                                                                                               555 CTATTGCTGCAAAGTCTTGAGAAGTCTAGGTCTTATGGATCTCCTTTTTCTCCTCAGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                             APCTACTGTCTCTACCCTGTAACTGGTATCTTCATGACATCTCGAAATATTTCCAAFTTCT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 23.5%; P
25; Conservative 154;
                                                                                                              /organism="Drosophila melanogaster"
/organism="taxon:7227"
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/clone=ib="kRPCI-98"
/clone_itb="kRPCI-98"
/clone_itb="kRPCI-98"
/note="end: TET3" 177 t 393 oth
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pred. No. 0.0
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                                                                                                                                                                                 AAWATAAATWTWWTWWTTYTTWAAWATAAAMCMAAWYYHTYTTYTYHYYTYWTYTMTWHY
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                                                                                                                                 CTGTAACTGGTATCTTCATGACATCTCGAATATTTCCCAATTTCTCTATTGCTGCAAAGTC
                                                                                                                                                                                                                           GCTATAGAGATAATTTCATGCACTATAGCTTTCAGTACTATCGTATCTACTGTCTCTACC 510
                                                                                         HTMYTHAWAHTTWYHWYHTYAMWHWMTWHWTMWAWWHWTTYTAAYYYYYTCMYYYHYMHW
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/note="end : TET3"
64 c 131 g
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/db_xref="taxon:7227"
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63 TATGAGATCCAGTGACAAGCTCATCTCTAGATGTCTGCATACCAATAAGTGACCCATCAT 122

THHKWMWTYNCRYKCHYNMYNYMTCHMTCCMYCHCWCCMCWCWHAWMWMWHWWHWAWAWV 985

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                                                                                                                                                                                                                                                                                                    - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MF project grant. The DNA was prepared from embryos by Alain Buch and Genevieve Payan. It has been constructed in the vector
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                        Similarity
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      Conservative 184;
                                                                                                   /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
108 c 131 g
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/db_xref="taxon:7227"
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                        3.7%;
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    ced. No. 0.00024;
Mismatches 175;
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BACN03K20 of DrosBAC library from
fly), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 WNW GENOSCOPE.CRS.fr)

- Web : Www.genoscope.Crs.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS0106X
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                                         Conservative
                                                                                                                                   /clone="BACN03K20"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
a 107 c 60 g :
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            Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; on bw Sp, the same Strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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                                                                                                                                                                                                                                                                                                                                 Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f.
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74; Conservative 147;
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AL108171
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Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Brachycera; Muscomorpha;
Enkaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Reveryota; Brachycera; Drosophila.
Ephlydroidea; Drosophila.
Ephlydroidea; Drosophila.
1 (bases 1 to 1101)
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : 1919 1006 EVRY cedex : FRANCE (E-mail : seqref@genoscope.cns.fr)
BP 191 91006 EVRY cedex : France : seqref@genoscope.cns.fr)
BP 191 91006 EVRY cedex : Genoscope.cns.fr)
Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Cetermination of this BAC-end sequence was carried out as part of a genoscope.cns.fr)

- Cetermination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project EBAC
- Collaboration with this Indian growided by a MRC
- Ilbrary (Dros BAC) was made by Alain Billaud at CEPH (Centre http://www.edgp.ebi.ac.uk - This Drosophila from embryos by Alain Bucheton d'Etude du Polymorphisme Humain) with finding provided by a MRC
- Ilbrary (Dros BAC) was made by Alain bucheton d'Etude du Polymorphisme Humain) with finding provided by a MRC
- Ilbrary (Dros BAC) was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton project grant.
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/organism="taxon:7227"
/dbox=ef="taxon:7227"
/clone="BACROJJ16"
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pred. No. 0.0088;
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SOURCE
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AUTHORS
TITLE
JOURNAL
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Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse

Recoptera; Endopterygota; Diptera; Brachycera;

Ephydroidea; Drosophildae; Drosophila.

Ephydroidea; Drosophila.
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                                                                                                                      Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of the project in the Berkeley Drosophila genome project (BDGP)

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope
Direct Submission
                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns fr
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Insecta; pterygota; era; muscomórpha;

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437 TCCACATATCTAAAGCTATAGAGATAATTTCATGCACTATAGCTTTCAGTACTATCGTAT 496
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                                                                                                                                                                                                                                                                                                                                                              617 GGTCTCCACACACCATTCACACTTCTTGAATATTCTTTGAACATAACAAATTCTCTCCAT 676
                                                                                                                  1067 УАММИНТАММААММИХИМИНАМАХНАННМИННИТ 1100
                                                                                                                                                                                                                             947 УҮННҮҮМТҮСТҮСНСҮАТЖҮМАМҮННМЖМАНИМНЖИНАНҮМИНҮМИТТҮҮТЖИММИМАҮА 1006
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                                                                                                                                                                                                                                                         TCATCTCTGCTTTGGTCATTCAAATCTCAAATGTAGCCATTTCTAAAAGGCTCTCCAAGA 796
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                                                                                                                                                                                                    GAATAATATTTGAAAGCATTTTGCTATTCTATCAAGTGATCATACAATGTCTGCTGCTCCTGC 856
                                                                                                                                                CACCACCATGACCATCCCCATGAATACAGACACT
1101 bp DNA linear GSS 03-JUN-1999 CMS CONTROL OF THE SECONDAL MELANGUAGE PROPERTY FROM DROSOPHILA MELANGUAGE (fruit BACROIM22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xre!" - (axx): (clone="hacN37F10" /clone_1ib="DrosBAC" /clone_1ib="DrosBAC11" /plasmid="peloBAC11" /plasmid="note="end" sp6" /note="end" 159 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164; Mismatches
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Pred. No. 0.
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                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTTCTCWTCATTTTCWMAMHMTMTAAWHYAYTTTMTTTTHATMWHMMWTTAYWTTMTWA 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              АТЫҰЫНАЫЫТТҰМҰАННТТТҮМҰНМНТҰТЫМСАМТМҰТҰМЫНСАСМТМТТЫТНЫНЫ 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCAMATTHTTTTTTTTTTTTTTTYYYYYYYYYMAMAMMYMAMTTTTYW 730
                                                                                                                                                                                                                                            Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Drosophilidae; Drosophila.
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as par-
collaboration with the EUC-end sequence project (ED
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS018ZP 1101 bp DNA linear GSS 26-JUL-1: Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 15ogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at the terminal than the BACPAC Resource Center can be
                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL108811.1 GI:5629115
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Location/Qualifiers
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/db_xref="taxon:7227"
/db_cref="taxon:7227"
/clone="BackRO1M22"
/clone_lib="RPCI-98"
/note="end : TET3"
162 c 148 g 177 t 281
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20.8%; Pred. No.
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RPCI-24-210F14.TJ
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97; Conservative
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              Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
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Mouse BAC
                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                         Mus musculus
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/clone_1ib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
End Sequences from Library RPCI-24
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/db_xref="taxon:7227"
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Sciurognathi; Muridae.
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                                            Shatsman, S., Akinret, B.,
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                                                                                                            Contact: Shaying Zhao, William Nie
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                           Unpublished (1998)
Other_GSSs: RPCI11-93G5.TJ
                                                                                                                                                                                                                     Berry, K., Granger, D., Suh, E., V
Use of human BAC End Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ321637 558 bp | RPCI11-93G5.TV RPCI-11 Homo sapiens
    Clones are derived from the
                                             9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                     Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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AQ321637
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Seq primer: SP6
Class: BAC ends.
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9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhao@tigr.org
Clones are derived from the mouse BAC_library RPCI-24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (pdejong@mail.cho.org).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ibrary availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                  (bases 1 to 558)
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector of the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-24"
/sex="Male"
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/clone="RPCI-24-210F14"
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human BAC library RPCI-11. For BAC
                                                                                                                                                      Nierman, Mark Adams
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAG--GCCCCAAGGGGTGAATCCATTTACTTACTTTTTCAGCTTCTAGTAGATGACC
                                                                           please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                             Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Beckeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fly), genomic survey sequence.
AL059199
AL059199.1 GI:4946662
GSS.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1031)
and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope.
Direct Submission
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
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/clone="RPCI-11-93G5"
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                                                                                                                                                                                                                                                                                                                                      722 УССМУУУУДАНТМАМИНАМТАССАТАЮСТИУАТИМИМАМИСУАНУАМУМИСММАСИСАУ 663
                                                                                                                                                                                                                                                             602 НТТНАТАТТИМАЛАЛАМТААТАМУМАЛАМТАМТАТМАМАЛАМИЛАНАЛАМАЛНАНАЛУЛА 543
                                                                                                                                                                                                                                          547 CAATTTCTCTATTGCTGCAAAGTCTTGAGAAGTCTAGGTCTTATGGATCTCCTTTTTCTCCT 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATGATTTTACCCATTTCCCCTCCATGGCACTCAACTCTCCTCTTCCTATGTGACCCTA 246
                                                                                                                                              422 GGHMAMCCCYGHCWMYYCWCACACAATTYAWAKCGDGGWSBABTMHHHAYNYTYTSTTAW 363
                                                                                                                                                                                       482
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11arity 22.1%; Pred. No. 0.06
1.1arity 198; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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/note="end : TET3"
/note="end : 124 g 214 t 348 oth
                    sequence.
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CIT-HSP-2378A6.TR CIT-HSP Homo s
  Homo sapiens
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Unpublished (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2378A6.TF
Other_GSSs: CIT-HSP-2378A6.TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 AAAGTTGAGTAACAGAGAAGAATCTTCCAGGAAACAGCTTAGACTCATTTTGTCCCCCATT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 458)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Adams, M.D., Rounsley, S.D., Zhao, S., Shizuya, H., Simon, M. and Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Barry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Barry, K., Golden, K., Shizuya, H., Simon, M., and Shizuya, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1145 TCTGACACCAGTTTCAATGTTTAG 1168
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TADAGCAGGAAAAATAATAATAATCTTTTCACAGTGGCACCTACATTCACTGGCAAAAGG 224
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                                                                                                                                                                                                                                                                                                                                              DNA linear GSS 03-JUN-1999 DNA linear GSS 03-JUN
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milarity 48.5%;
Conservative
Drosophila melanogaster.
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota,
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
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/note="Vector: pBeloBAC11; Site_1: HindIII;
/note="Vector: pBeloBAC11; Site_1: HindIII;
HindIII"
70 c 92 g 128 t 2 others
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                                                                                                                         WMWMY AHTHAWTMY NCTMTAWWTMT AACWAAWAAAHTTTTT AY AATMTHTCATMTWCN
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TCTCCACACCATTCACACTTCTTGAATATTCTTTGAACATAACAAATTCTCTCCATGG
                                        TWTACWTAMMYMTMHMCMMHMAYMTMCCMCACMCTCATMTATAYHCTCYTWHTMTCNCTW
                                                                                                                                                                GTCTCTA----CCCTGTAACTGGTATCTTCATGACATCTCGAATATTTCCAATTTCTCTAT
                                                                                                                                                                                                                                                 ATATCTAAAGCTATAGAGATAATTTCATGCACTATAGCTTTCAGTACTATCGTATCTACT 501
                                                                                                                                                                                                                                                                                                                                                                         HTAATAWCWYHTACAHACAHTYTCTCTMCWTAYATCATAMCMTMAHATAATATMTMTATM
                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTHCCYCHTAYAHMMYMTWCACACTTMYAYTMNACTCWTMTMTAMNMTWMAAWAYHAAWA
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                                                                               TGCTGCAAAGTCTTGAGAAGTCTAGTCTTATGGATCTCCTTTTCTCCTCAGGTCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                               TTTCCCCTCCATGGCACTCAACTCTCCTCTTCCTATGTGACCCTACTTATGTCCTATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic Strain y2; on bw sp, the same strain used for the BDGP's partial and Permittee a more detailed description of the BDGP's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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/db_xref="taxon:7227"
/clone="BACR30118"
/clone_lib="RPCI-98"
/note="end: TET3"
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420 ACACTTTCTCCTCATAATCCACATATCTAAAGCTATAGAGATAATTTCATGCACTATAGC
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                                          TMMTAMY MTAMTTMMMMCTMMMTMMMMMMMMMHMTTMHTMTTAMTMAMTMT - MTMTMT
                                                                                 TCACTCACAGTTTCTTGAGAGCAGAAGACTCAGAACTGATCTGTCCTCAATGTCCTCCCT 419
                                                                                                                            AAMAAAMATHTTMTTTTAMATTMMTTTAMTMAMTTMATMTTTYMMTMTTMCTMCTMTTTC
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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/note="end : T7"
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                                                                                                                   679 MAAMMUMTMINAIMINAAMITAIMAMNITAIAMITAWAAWAAIAMAAMIAAITAITAITWI 620
                                                           600 TTCTCCTCAGGTCTCCTGGTCTCCACACACCATT 633
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ACUVALTO HOMO SAPI
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RESULT 1
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
                                                                                                                       DEFINITION
                                                                           Mus musculus
EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
1 (bases 1 to 219386)
1 (bases 1 to 219386)
McPherson, J.D. and Waterston, R.H.
McPherson, J.D. and Waterston, R.H.
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Sequencing vector: M13, 0%

Sequencing vector: plasmid; 100%

Sequencing vector: plasmid; 100% of reads
Chemistry: pye-terminator Big Dye; 100% of reads
Chemistry: bye-terminator Big Dye; 990319

Chemistry: bye-terminator Big Dye; 990319

Chemistry: bye-terminator Big Dye; 990319

Chemistry: bye-terminator Big Dye; 900319

Chemistry: bye-terminator Big Dye; 900319

Consensus quality: 216712 bases at least 030

Consensus quality: 216719 bases at least 030

Consensus quality: 216719 bases at least 020

Consensus quality: 216719 bases at least 020

Consensus quality: 216719 bases; agarose-fp
Insert size: 171980; sum-of-contigs
Ouality coverage: 11.97 in 020 bases; sum-of-contigs
Ouality coverage: 11.97 in 020 bases; sum-of-contigs
Ouality coverage: 11.97 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary, but the exact sizes of the gaps are unknown arbitrary will be updated with the finished sequence runs of N, but the exact sizes of the finished sequence runs of will be updated with the finished sequence as soon as it is available and the accession number will as soon as it is available and the accession number will be recorded.
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3t. Louis, MO 63108, USA

2002 this sequence version replaced gi:21490647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               grved. 105: contig of 105 bp in length

205: gap of unknown length

806: contig of 601 bp in length

906: gap of unknown length

5269: contig of 4363 bp in length

5369: gap of unknown length

16393: contig of 11024 bp in length

16393: gap of unknown length

16493: gap of unknown length

16493: gap of unknown length

80451: contig of 1694 bp in length

80845: contig of when the service of 1818 bp in length

18045: gap of unknown length

18045: gap of unknown length

18045: contig of 57297 bp in length

138342: contig of 81044 bp in length

138342: contig of 81044 bp in length.
                                                                                                                                                        /note="assembly_name:Contig14"
907. .5269
                                                                                                                                                                                                                                                                                                                             /chromosome="UNK"
/clone="RP24-350A15"
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                /note="assembly_name:Contig19" 5370. .16393
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Db 126817 AAATGTTCCCTTTGCAGAAGCAATCTTAATCCCTCTTTTAGCACACTTGATGTGATCTTT 126876
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Best Local Similarity
Matches 1345; Conserv
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                                                                                          AGACTGAAAAGTCAATGAATAGAGGACTCCACTCAGGGGAAGCTCGGATGGGTGTGTTTTG
                                      ACCTGCAGGGATTCTGAAGCTGGGCTCTTCTGTCCGCAGGACGGTGTTCTGAATGCCACA 840
ACCACGCCACCTGCACGGTGGATGGTGTGGTCACAACGTGCTCCTGCCAGACCGGCTTCA 900
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34752. 80845
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80946. 138242
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138343 . 219386
/note="assembly_name:Contig24"
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| 1141 | CCGAGGGCTTTACAGGGGATGGTTGGTACTGTGAGTCCCCAGGCTCCTGTGAGCCAG 127896
| 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 | 1141 
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ince i (pases i to lbb03) adio-oduola, B., Ali-osman, F.R., Allen, C., Arey, J.R., Ayele, M., Banks, T., Asprooks, S.L., Amaratunge, H.C., Arey, J.R., Ayele, M., Banks, T., Barbooks, S.L., Amaratunge, H.C., Arey, J.R., Ayele, M., Banks, T., Barbooks, S.L., Bankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., E., Brown, M., Bryant, N.P., Bouck, J., Bowie, S., Brieva, M., Brown, C., Chacke, J., Coyle, M.D., Darborne, S.R., Christopoulos, C., Coyle, M.D., Dathorne, S.R., Chen, R., Chen, R., Coyle, M.D., Dathorne, S.R., Christopoulos, C.C., Chen, R., Cohen, R., Chen, R., Dathorne, S.R., Durbin, K., M., Davis, C., Davy-Carroll, J., Dederich, D., A., Chen, R., Chen,
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Rattus norvegicus
Rattus norvegicus; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
Mammalla; Eutheria; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18701283.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 74 contigs. The true order of the pieces

* to mot known and their order in this sequence record as

* is not known and their order in this sequence as

* is not known and their order in this sequence as

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* arbitrary but the exact sizes of the gaps are unknown.

* this record will be updated with the finished sequence

* as soon as it is available and the accession number will

* as soon as it is available and the accession number will
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Center project name: GMMD
Center clone name: CH230-142F15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
contact: hpsc-help@bcm.tmc.edu
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                                                                                                                                                                                                            CTCAGATATGCACGGCTGGTACCGG 135105
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                                                                                                                                                                                                                                                                                   ATATGAGACCCTGACTGAGTACTGGCGCACAGAGAGTATGGTGTGGGCTACTCCTGTGA 1321
                                                                                                                                                                                                                                                                                                                                                                                     TAACTGTCATTCCCTGGCTACCTGTGTCAACACGCAAGGCAGCTACTCATGCGTGTGTCC
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Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                 AC110401 187332 bp | Rattus norvegicus clone CH230-41K9,
                                                           HTG; HTGS_PHASE1.
                                                                       AC110401.3 GI:21738952
                                                                                                     56 unordered pieces
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                                                                                                                                                                                                                                                                                                        Worley, K.C
   Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 149700 bases at least 030
Consensus quality: 156256 bases at least 030
Consensus quality: 162284 bases at least 020
                                                                                                                                                                                                                                                                                                                            (bases
                                                                                                                                                                                                                                                                                                                                                                                                                (bases
                                                                                                        Center project name: GRHP
Center clone name: CH230-41K9
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Carron, Full, F., Burkell, C., Bultfell, K.L., Byrd, N.C.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Dinny, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Garrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Miner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Peters, L., Pickens, R., Primus, E., Py, L.L., Okuwonu, G.
Oragunye, N., Nickerson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Wulliamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wulliamson, A., Wleczyk, R., Wooden, S., Watlington, S.,
Direct Submission
                                                                                                                                                                                                                      Direct Submission
Submitted (13-UTI-2002) Human Genome Sequencing Center, Depoi Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18847066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
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(bases 1 to 187332)
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least Q40 least Q30 least Q20

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence as soon as it is available and the accession number wibe preserved.
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NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Contact: Capabs -remail.nih.gov
Email: cgapbs -remail.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
Tissue procurement: Jeffrey Greenhologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
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LPQGPDGKLVCQDPCNTYETLTEYWRSTEYGVGYSCDAGLHGWYRFTGQGGVRMAETC
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Tamm-Horsfall; uromodulin.
Mus musculus cDNA to mRNA.
Mus musculus
                                                                                                     (Tamm-Horsfall
                                                                       Nucleotide
                                                                                  Kumar,S
                                                                                         Prasadan, K., Bates, J.,
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∕organism≃"Mus musculus
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LTAAPBECNLAYCTDPSSVEGTCEECRYDEDCISDNGRWRCQCKQDSNITDVSQLEYRL
ECGANDIKMSLRKCQLQSLGFWNVFMYLNDRQCSGFSESDERDWMSTVTPARNGPCGT
VLERNETHATYSNTLYLANAIIIRDIIIRMNFECSYPLDMKVSLKTSLQPMVSALNIS
LGGTGKFTYRMALFQSPTYTQPHQGPSVMLSTEAFLYVGTMLDGGDLSRFVLLMTNCY
ATPSSNSTDPVKYFIIQDSCCRTEDTTIQVTENGESSQARFSVQMFRFAGNYDLYYLH
CEVYLCDSTSEQCKPTCSGTRFRSGNFIDQTRVLNLGPITRQGVQASVSKAAASSNLRL
LSIWLLLFPSATLIFMYQ"
576 c 603 g 520 t
                                                     sequence and peptide motifs of mouse uromodulin fall protein)-the most abundant protein in mamma
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Pred. No. 7.9e-143;
0; Mismatches 3;
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                                328-332 (1995)
                                                                                        Dell, M., Sukhatme, V.,
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/prodein_id="AAA73896.1"
/protein_id="AAA73896.1"
/protein_id="AAA73896.1"
/db_xref="GI:927203"
/translation="MGIPLIFWMLLVMMVTSWFTLAGASNSTEARRCSECHNNATCTVD
GVVTTCSCQTGFTGDGLYCEDMDECATPWTHNCSNSSCVNTPGSFKCSCQDGFRLTPG
GVVTTCSCQTGFTGDGLYCEDMDECATPWTHNCSNSSCVNTPGSFKCSCQDGFRLTPG
GVVTTCSCQTGFTGDGLYCEDMDECATPWTHNCSNSSCVNTPGSGGWYCECSPSSCEDGLDC
LPQGPDGKLYCQDPCNTYETLTEYWRSTEYGYGYSCDAGGHGWYRETGOKGGVQRNAETC
VPVLACNTAAPMWLMGSHPSSSEGIVSRTACAHWSDHCCRWSTEIOVKACPGGFY I'N
LTEPPECNLAYCTDPSSVEGTCEECRVDEDCISNGRWRCQCKQDSNITDVSQLEYRL
ECGANDIKKSLRKCQLOSLGFMNVFMYLNDRQCSGFSESDERDMMSI VTPARNGPCGT
VLRRNETHATYSNTLYLANAIIIRDIIIRMDECSGFSESDERDMMSI VTPARNGPCGT
VLRRNETHATYSNTLYLANAIIIRDIIIRMDECSGFSESDERDMSSLVTPLMTNCY
ATPSSNSTDPVKYFIIQDSCPRTEDTTIQVTENGESSQARFSVQMFRFAGNYLLYYLH
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Bovine and rodent tamm horsfall protein (THP) genes: cloning, structural analysis, and promoter identification gene Expr. 4 (1-2), 63-75 (1994) 95113938.
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Mammalia; Eutheria;
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TGCTCCCAGGCTCCTGTGAGCCAGGACTGGACTGCCTTGCCCCAGGGCCCGGATGGAAAG 1235
                                                                sp. kidney.
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/db_xref="taxon:10118"
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Pred. No. 9.6e-115;
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Sciurognathi; Muridae; Murinae;
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RATUROMOD
Rat Tamm-Horsfall protein mRNA,
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Mammalia; Eutheria;
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/translation="McQLLSLTWLLLVMYVTPWFTHCSNSICMNTLGSYECSCODGERLT
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LDGVVTTCSCOAGETGDGLYCEDIDECATPWTTGGSYSCVCPKGYRCDGWYCECSPGGECPGL
LDGVVTCSCOAGETGDGLYCEDIDECATPWTTGGSYSCVCPKGYREDGWYCECSPGGETY
PGLGCLDVNECTEQGLSCHCHSCATCYNTAGATSTEIOVKACPGGTY
DCLDVLRCNTAAPMILAGSHPSSREGIYSRTDYGAGYSCDSDMHGWYRETGOGGYNMAE
TCVPVLRCNTAAPMILAGSHPSSREGIYSRTDVGAGYSGCKGDENWIGIVTPARDGEC
YNLTEPPECNLAYCTDPSSVEGTCEGCTWENCOKGSEGERDMASIVTPARDGEC
YNLTEPPECNLAYCTDFSSVEGTEYTOLSLGFMKVPMYLNDRGCSGFSERGERDMASIVTPARDGEC
RICCHTATYSMTYLASEIITRDINIRINEECSYFLDMYSLKTSLOPMYSALN
GTVLRRNETHATYSMTLKLASEIITRDINIRINEECSYFLDMYSLKTSLOPMYSALN
GTVLRRNETHATYSMTYLDAYCHTCDTTTQVTENGESSOARFSLGMFRFAGNSDLVY
CYATPSSNSTDPVKYFIIQDFRCPHTEDTTTQVTENGESSOARFSLGMFRFAGNSDLVY
GFLSTWLLLFLSATITLMYH"
GFLSTWLLLFLSATITLMYH"
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/db_xref="taxon:10116"
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/product="uromodulin"
/protein_id="AAA42319.1"
/protein_id="AAA42319.1"
/db_xref="GI:207621"
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88.1%;
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Rodentia; Sciurognathi; Muridae; Murinae;
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pred. No. 9.6e-115;
pred. No. 63;
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
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AC106796
AC106796.2 GI:22122880
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-AUG-2002) Production Sequencing Facility, DOE Jo Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, On Aug 6, 2002 this sequence version replaced gi:18139346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-JAN-2002) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut 3 (bases 1 to 16887)
DOE Joint Genome Institute.
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
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Base-by-base quality values are not generally visible from GenBank flat file format but are available as part
                                                                                                                                                                                                                                                                        Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible GenBank flat file format but are available as part of this entry's ASN.1 file.
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                                                                                          entry's ASN.1 file.
 /organism="Homo sapiens"
/db_xref="taxon:9606"
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ne 16 clone RP11-429K17, complete sequence.
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3498215
                                                                                                                                                                                                                                                                                                                             Human uromodulin (Tamm-Horsfall glycoprotein) mRNA, M17778
                                                                                                                        Mattaliano,R.J., Tizard,R., Kawashima,E., Schmeissner,U., Heletky,S., Chow,E.P., Burne,C.A., Shaw,A. and Muchmore,A.V. Uromodulin (Tamm-Horsfall glycoprotein): a renal ligand for
                                                                                                                                                                                                                                                                        Tamm-Horsfall glycoprotein; glycoprotein; uromodulin Human kidney, cDNA to mRNA, clone 6.7\,\cdot
                                                                                      Science 237
                                                                                                                                                                               1 (bases 1 to 2290)
Hession, C., Decker, J.M., Sherblom, A.P., Kumar, S., Yue, C.C.,
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/organism="Homo sapiens'
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Nutheria; Primates;
                                                                                        (4821), 1479-1484 (1987)
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Pred. No. 7.1e-80;
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Sequence 6590 from Patent W00194629.
AX336081
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GLGCTDVDECAEPGLSHCHALATCVNVYGSYLCVCPAGGYYCVCP
CVPEGDALVCADPCQAHRTLDEYWRSTEYGGGFACACTGVYGCGGARNAETCV
PVLRCNTAAPMMLNGTHPSSDEGIVSRKACAHWSGHCLVDASVQVKACAGGYYVYNL
PVLRCNTAAPMMLNGTHSSDEGIVSRKACAHWSGHCCCKODENITDISLLEHRLE
TAPPECHLAYCTDPSSVEGTCEECSIDEDCKSNNGRWHCQCKODENITDISLLEHRLE
TAPPECHLAYCTDFSSVEGTCEECSIDEDCKSNNGRWHCQCKODENITDISLLEHRLE
TARNETHATTSNTLYLADEIIIRDLNIKINFACSYPLDMKYSLKTALOPMVSALMIRV
CGANDMKVSLGKCQLKSLGFDKVFMYLSDSRCSGFNDRDNKVSLKTALOPMVSALMIRV
LTRRETTHATTSNTLYLADEIIIRDLNIKINFACSYPLDMKYSLKTALOPMVSALMIRV
GGTGMTTVRNALFQFDSYTQPYGGSSVTLSTEAFLYVGTMLDGGDLSRFALLMTNCYA
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TPSSNATDPLKYFILOTGGGTRFRSGSVIDQSRVLNLGPITRKGYQATVSRAFSSLGLLK
EVYLCDTMNEKCKPTCSGTRFRSGSVIDQSRVLNLGPITRKGYQATVSRAFSSLGLLK
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bp downstream of 5' end of mRNA.
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106. .2028
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/db_xref="GI:340166"
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Pred. No. 6.6e-72;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Horrigan, S., Soppet, D.R. and Weaver, Z.
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Location/Qualifiers
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Sequence 6855 from Patent WO0194629
AX336346
young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
                                          Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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/db_xref="taxon:9606"
692 c 673 g 49
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Pred. No. 6.6e-72;
                                              Chordata: Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Sequence 7209 1
Ax336700
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                                                                                         Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic scree
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Patent: W
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
692 c 673 g 49
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
692 c 673 g 49
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from Patent W00194629
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Pred. No. 6.6e-72;
0; Mismatches 132;
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Pennica,D., Kohr,W.J., Kuang,W.J.,
Chen,E.Y. and Goeddel,D.V.
Identification of human uromodulin
                                                                                                                                                                                                                                                                                                   Homo sapiens
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Human uromodulin (Tamm-Horsfall
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                                                                                                                                                                                    Science 236 (4797),
                                                                                                                                                                                                     glycoprotein
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Tamm-Horsfall glyco
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                                                                                                                                                                                                                                                                                                               orsfall glycoprotein; glycoprotein; uromodulin cDNA to mRNA.
/protein_id="AAA36798.1"
/protein_id="AA336798.1"
/db_xref="GI:340164"
/translation="MGQPSLTWMLMVVVASWFITTAATDTSEARWCSECHSNATCTED
EAVTTCTCQEGFTGDGLTCVDLDECAIPGAHNCSANSSCVNTPGSFSCVCPEGFRLSP
                                                          /note="uromodulin precursor"
/codon_start=1
                                                                                       169. .2091
                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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73.5%;
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Pred. No. 6.6e-7
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                       AK091961 2408 bp Homo sapiens cDNA FLJ34642 fis,
                                                                                          oligo capping; fis (full insert sequence).
Homo sapiens kidney cDNA to mRNA, clone_lib:KIDNE2
                                                                                                                        AK091961.1 GI:21750445
                                                                                                                                           AK091961
                                                                                                                                                       to UROMODULIN PRECURSOR.
                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                Homo sapiens
                                                                              clone:KIDNE2016918.
   Tashiro, H.,
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CVPEGDALVCADPCQAHRTLDEYWRSTEYGEGYACDTDLRGWYRFVGQGGARMAETCV
PVLECNTAAPMWLNGTHPSSDEGIVSRKACAHWSGHCCLWBASYQVKACAGYYVYNL
PVLECHAYCTDPSSVEGTCEECSLDEDCKSNNGRWHCQCKQDFNITDISLLEHRLE
TAPPECHLAYCTDPSSVEGTCEECSLDEDCKSNNGRWHCQCKQDFNITDISLLEHRLE
CGANDMKVSLGKCQLKSLGFDKVFMYLSDSRCSGFNDNRDWYSVYTPAADBCPCGTV
CGANDMKVSLGKCQLKSLGFDKVFMYLSDSRCSGFNDNRCWYSVTPAADBCPLNTRV
LTRNETHAATYSNTLYLADEIIIRDLNIKINFACSYPLDMKVSLKTALQPMVSALNIRV
GGTGMFTVRWALFQTESYTQPYQGSSVTLSTEAFLYVGTMLDGGDLSRFALLMTNCYA
GGTGMFTVRWALFQTESYTQPYQGSSVTLSTEAFLYVGTMLDGGDLSRFALLMTNCYA
CTPSSNATDPLKYFIIQDRCPHTRDSTIQVVENGESSQGRFSQQMFRFAGNYDLVYLHC
TPSSNATDPLKYFIIQDRCPHTRDSTIQVVENGESSQGRFSVQATVSRAFSSLGLLK
EVYLLDTMNEKCKFTCSGTRFRSGSVIDQSRVLNLGPITRKGVQATVSRAFSSLGLLK
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241..2
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Pred. No. 6.6e-72;
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                                      Primates;
                                                   Chordata;
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      Watanabe, K.,
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                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                               mRNA linear
clone KIDNE2016918,
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         Kumagai,A., Itakura,S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGTGCACCTGTCAGGAGGCCTTCACCGGCGATGGCCTGACCTGCGTGGACCTGGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan Kazusa-Kamatari, Cojp, Tel:81-438-52-3975, Fax:81-438-52-3986) (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) (E-mail:genomics@hri.co.nd) Faxis project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: RAB, Rey Technology Center (HRI) (supported by Japan construction: Helix Research Institute (HRI) (supported by Japan Kay Technology Center etc.); 5'-6 3'-end one pass sequencing: RAB, RAB; and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                           GTGGATGAGTGCGCTGAGCCTGGGCTTAGCCACTGCCCACGCCCTGGCCACATGTGTCAAT
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NEDO human cDNA sequencing
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ACAGAGTATGGTGTGGGCTACTCCTGTGACGCGGGTTTGCACGGCTGGTACCG 1345
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/db_xref="taxon:9606"
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                                                                                                                                                        933 GAGTGTGCTACCCCATGGACTCACAACTGCT----CCAACAGCAGCTGTGTGAACACCCCCG
                                                                                                                                                                                                                                                                                                               205
                                                                       GGCTCGTTTAAGTGCTCCTGTCAGGATGGTTTTCGTCTGACGCCTGAGCTGGAGCTGCACT 1049
                                                                                                                               GAATGCGCCGTTCTGGGGGGCGCACAACTGCTCCGCCACCAAGAGCTGCGTGAATACGCTG
                                                                                                                                                                                                                                                                                                      TCAGCAAAAAGCTGCTCTGAATGTCACAGCAATGCCACTTGTACGGTGGACGGGGCTGCC
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                                          GGCTCTTACACGTGCGTCTGCCCTGAAGGTTTTCTCCTGAGCTCGGAGCTCGGCTGCGAG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 161877] from the original journal article. This sequence comes from Fig. 2A.

Location/Qualifiers
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Yu.H., Papa,F. and Sukhatme,V.P.

Bovine and rodent tamm-horsfall protein (THP) genes: cloning, structural analysis, and promoter identification

Gene_Expr. 4 (1-2), 63-75 (1994)
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1 (bases 1 to 2340)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCEVYLCDTVNEKCRPTCPETRFRSGSIIDQTRVLNLGPITRKGGQAAMSRAAPSSLG
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TVMTRNETHATYSNTLYLADEIIIRDLNIRINFACSYPLDMKVSLKTSLQPMVSALNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLQVWLPLLLSATLTLMSP"
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/db_xref="GI:912815"
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/note="This sequence comes from Fig.
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/db_xref="taxon:9913"
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               AGCACAGAGTATGGTGTGGGCTACTCCTGTGACGCGGGTCTGCACGGCTGGTACCG 1345
                                                 GACGCGCTCGTGTGCACCCGTGCCAGCTGCACCGCATCCTGGACGACGAATACTGGCCGC
                                                                                                                                                    ATGGCGAGGCAACTACTCGTGCGTGTGTCCTGCGGGCTACCTGGGAGACGGAAGGCAC
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Search completed: February 17, 2003, 15:15:26 Job time: 4011.36 secs

Title: perfect score:

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2001
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February 17, 2003, 08:20:43; Search time 4997.09 Seconds (without alignments) updates/sec 11653.717 Million cell updates/sec

sequence: Scoring table:

IDENTITY\_NUC Gapext 1.0

2054640 seqs, 14551402878 residues

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Minimum DB s

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Total number of hits satisfying chosen parameters:

Run on: OM nucleic

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nucleic search, using sw model

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

## score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result 000  $\sigma$   $\sigma$   $\sigma$ No. WORDS URCE ORGANISM Score FERENCE AUTHORS TITLE ESSION US \_\_\_\_ NOITION 79.8 78.2 75.8 75.8 74.8 74.6 74.4 74.4 74.2 86 Query Match Length DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Mus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus 1 (bases 1 to 219386) 1 (bases 1 to 219386) McPherson, J.D. and Waterston, R.H. McPherson, J.D. and Waterston, R.H. AC125147.2 GI:21539180 HTG; HTGS\_PHASE1; HTGS\_DRAFT. house mouse. 7 135302 7 136073 7 1363190 7 172462 7 147212 5 113894 5 113894 5 113894 5 113894 5 113894 5 110397 5 130097 5 130097 5 1504876 6 220778 6 220778 6 220778 6 221982 6 241985 6 241985 6 237550 6 237550 6 237550 6 237550 6 237550 6 237550 6 237550 6 237550 7 158266 AC125147 AC110401 AC111518 AL831768 AL772289 AC177289 AC068493 AC123466 AC120738 AC121139 AC128306 AC121738 AC125498 AC125498 AL833789 AL808141 AC131362 AC122568 AC127923 AL772214 AC126053 ALIGNMENTS AC1125147 Mus muscu AC110401 Rattus no AC111518 Rattus no AC111518 Rattus no AC111518 Danio rer ALJ372289 Danio rer ALJ372289 Danio rer AC122456 Rattus muscu AC122455 Mus muscu AC122350 Kus muscu AC12437 Mus muscu AC12437 Mus muscu AC12439 Mus muscu AC12439 Mus muscu AC127103 Mus muscu AC127103 Mus muscu AC121603 Mus muscu AC121738 Danio rer ALB4471 Danio rer ALB33789 Mus muscu AC12458 Mus muscu AC1097097 Rattus no AC1097097 Rattus no AC1097097 Rattus no AC1095049 Rattus no AC095949 Rattus no A Description

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Consensus quality: 216121 bases at least Q40 consensus quality: 216506 bases at least Q20 Consensus quality: 216719 bases at least Q20 Insert size: 171000; agarose-fp Insert size: 217980; sum-of-contigs Quality coverage: 14.92 in Q20 bases; agarose-fp Quality coverage: 11.97 in Q20 bases; sum-of-contigs
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McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; 0% Sequencing vector: plasmid; 100%
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On Jun 22, 2002 this sequence version replaced gi:21490647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-JUN-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-JUN-2002) Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                          /note="assembly_name:Contig19" 5370. .16393
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                                                                                                                                                                                                                                                                   Location/Qualifiers
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contig of 601 bp in length
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                                                      CCTCTCCCCACCAGCTCTCTCTCTCTGTATATGCACATACACAGTGAGCTAGTGTGC
                                                                   CCTCTCCCCACCAGCTCTCTCTCTCTCTGTATATGCACATACACAGTGAGCTAGTGTGC
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/note="assembly_name:Contig22"
80946 138242
/note="assembly_name:Contig23"
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                                                                                                            TTGAACTCACTATGAAGCTAGCAATGACCTTGAGCTTCTGATCCTTATATCTACACTCTC
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Buhay, C., Burch, P., Burkett, C., Burch, K. L., Byrd, N. C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Chen, G., Chen, R., Chen, Z., Coyle, M. D., Dathorne, S. R., David, R.,
Davila, M. I., Davis, C., Davy, Carroll, L., Ding, Y., Dinh, H. H.,
Davila, M. I., Davis, C., Davy, Carroll, L., Ding, Y., Dinh, H. H.,
Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H.,
Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J.,
Earnhart, C., Edgar, D., Edward, C. C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Coster, N., Gill, R.,
Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E.,
Jacobson, B., Jla, Y., Johnson, R., Jolivet, S., Joudah, S.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L.,
Li, J., Li, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Manssey, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M.,
Massey, E., Martindale, A., Martindale, A., Martinez, E.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Morris, S.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N.,
Nguyen, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Sonale, T., Shoshtari, N., Sisson, I.,
Sodergren, E., Sonale, T., Shoshtari, N., Stanley, H., Stoone, H.,
Sonale, T., Sparks, A., Stanley, H., Stoone, H.,
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Tansey, J., Taylor, C., Taylor, T., Telifod, B., Thomas, N., Thomas, S.,
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Submitted (12-FEB-2002) Human Genome Sequencing Center, Depai of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 187332)
Submitted (13-JUL-2002) of Molecular and Human Baylor Plaza, Houston,
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                                                                                               Direct Submission
                                                                                                                            Worley, K.C.
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56 unordered pieces.
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   ) Human Genome Sequencing
Genetics, Baylor College
TX 77030, USA
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NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Center clone name: CH230-41K9
Center clone name: CH230-41K9
Center clone name: CH230-41K9
Center clone name: CH230-41K9
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 149700 bases at least Q40
Consensus quality: 156256 bases at least Q30
Consensus quality: 162284 bases at least Q20
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ACCESSION VERSION KEYWORDS

AC111518 AC111518.2 GI:21736068 HTG; HTGS\_PHASE1. RESULT 3 AC111518 LOCUS

DEFINITION

Rattus norvegicus clone CH230-142F15, \*\*\*, 74 unordered pieces.

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linear HTG 23-JUL-2002 SEQUENCING IN PROGRESS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 165503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                              Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Molecular Houston, TX 77030, USA Baylor Plaza, Houston, TX 77030, USA Divided this sequence version replaced gi:18701283. On Jul 12, 2002 this sequence version replaced gi:18701283. Center: Baylor College of Medicine Center: Baylor College of Medicine Center Code: BCM
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                                                                                   Web Site: http://www.hgsc.bcm.tmc
Contact: hgsc-help@bcm.tmc.edu
Contact: hproject Information
Center project name: GMMD
Center project name: CH230-142F15
Center clone name: CH230-142F15
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Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program Phrap; version 0.990329
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Rodentia; Sciurognathi; Muridae; Murinae;
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

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pred. No. 2.3e-157;
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ORGANISM
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AUTHORS
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JOURNAL
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                                                                                                                                                                                        unordered pieces.
                                                                                                                                                                    ALB31768.5 GI:22416172
HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1, Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Actinopterygii; Neopterygii; Danio. Cypriniformes; Cyprinidae; Danio. Cypriniformes; Cyprinidae; Danio.
                                Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, CBLO 15A, UK E-mail enquiries: zface@sanger.ac uk Clone requests: cloperequest@sanger.ac uk Clone requests sequence version replaced gi:22204775. On Aug 21, 2002 this sequence version replaced gi:22204775.
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                        DNA linear HTG 17-AUG-2002
SEQUENCING IN PROGRESS ***, 6
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator; 11% of reads
Chemistry: Dye-terminator Big Dye; 88% of reads
Chemistry: Dye-terminator Big Dye; 88% of reads
Consensus quality: 154355 bases at least Q40
Consensus quality: 155354 bases at least Q30
Consensus quality: 155364 bases at least Q20
Consensus quality: 155984 bases at least Q20
Insert size: 136454; sum-of-contigs
Insert size: 135094; 19.4% error; agarose-fp
Quality coverage: 6.55x in Q20 bases; sum-of-contigs Quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coverage: 8.69x in Q20 bases; agarose-fp
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59792 59891: gap of 100 bp
59892 88854: contig of 28963 bp in length
88855 88954: gap of 100 bp
88955 129451: contig of 40497 bp in length
129452 129551: gap of 1070 bp
129452 129533: contig of 20772 bp in length
150324 150423: gap of 100 bp
150424 154572: contig of 3634 bp in length
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/db_xref="taxon:7955"
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fragment_chain:1"
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1. .59791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: zface@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on aug 21, 2002 this sequence version replaced gi:21911683.
                                                                                                                                                                                                                                                             Insert size: 167453; sum-of-contigs
Insert size: 151375; 7.0% error; agarose-fp
Quality coverage: 6.21x in Q20 bases; sum-of-contigs Quality
coverage: 6.94x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 166878 bases at least Q20 Consensus quality: 165248 bases at least Q30 Consensus quality: 166878 bases at least Q20 Consensus quality: 166878 bases at least Q20
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1 (bases 1 to 168153)
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Danio rerio clone CH211-8A9,
                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently * consists of 8 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: zface@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: SC
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                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
1 6555: contig of 6555 bp in length
6556 6655: gap of 100 bp
6656 29673: contig of 23018 bp in length
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PROGRESS ***, 8
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TCTTTTGCTTCTGTGACCTCCACATATTCATTGAAGCGCAAAATTCTGCGTGCCACCAAT 14790
                                                                 CATCGTACTTTGTCTGCAGGGGTTAACCTAGTCCAGGGCTTGTCAGCACGTCGATCATAG 14730
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29774 65169: contig of 35396 bp in length
65170 65269: gap of 100 bp
65270 78612: contig of 13343 bp in length
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fragment_chain:3"
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78713. .
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/db_xref="taxon:7955"
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fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 256302 at least Q20
*Consensus quality: 254124 at least Q30
*Consensus quality: 250276 at least Q40
*Stimated insert size: agarose-FP - N/A
Charlet of the control of th
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Montgomery, K. T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R. Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R.
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Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E.,
Gordon, M., Goltz, J.S. and Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hpcgg.org/Sequence/mouse.html
Contact: hpgc@mendel.mgh.harvard.edu
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On Aug 11, 2001 this sequence version replaced gi:14993654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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51730: contig of 51730 bp in length 51750: gap of unknown length 82423: contig of 30673 bp in length 82443: gap of unknown length 118158: contig of 35715 bp in length 118178: gap of unknown length 139441: contig of 21263 bp in length 139441: gap of unknown length 160638: contig of 21177 bp in length 160658: gap of unknown length 177611: contig of 16953 bp in length 177631: gap of unknown length
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C57BL6/J, WORKING DRAFT
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                                                                        /note="assembly_name:Contig129"
220794. .229643
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                                                                                                                                                                            177632. .19099:
                                                                                                                                                                                                                                                                                                     /note="assembly_name:Contig138" 51751. .82423
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                                                                                                                                                  /note="assembly_name:Contig132"
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/clone="RP23-76K1"
                                 /note="assembly_name:Contig127"
                                               /note="assembly_name:Contig128"
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                                                                                                                                                                                   /note="assembly_name:Contigl33"
                                                                                                                                                                                                                                                                                                                                         /sex="male"
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                                                                                                                                                                                                                                   note="assembly_name:Contig135"
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 e="assembly_name:Contig126"
69. .249725
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g of 2856 bp in length
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AC123466 179047 bp 184718 norvegicus clone CH230-18J2, 67 unordered pieces.
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*** SEQUENCING IN PROGRESS ***,
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TITLE
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Douthwaite, K. J. Draper H., Dugan-Rocha, S., Durbin, K. J.,
Earnhart, C., Edgar, D., Edwards, C. C., Elaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E.,
Jacobson, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L.
Li, J., Li, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Massey, E., Mawhiney, E., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Morgan, M., Morris, S.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Pitchens, C., Shen, H., Shooshtari, N., Sison, I.,
Sodergren, E., Sonaike, T., Spark, A., Tamerisa, A., Tamerisa, N., Tamerisa, N., Tomas, S.,
Williams, G., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Direct Submission
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Submitted (23-JUL-2002) Human Genome Sequencing Center, Depa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Baylor Plaza, Houston,
3 (bases 1 to 179047)
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                                                                           Center project name: CH
                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is
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be preserved.
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Sequence 14 from patent US 5670367.
166494
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Turbase 1 to 7218)
Torner, F., Scheiflinger, F. and Falkner, F. Gunter.
Toorner, F. and Falkner, F. Gunter.
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Mus musculus chromosome UNK clone RP23-76C13, WORKING DRAFT
SEQUENCE, 49 unordered pieces.
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                                    Mus musculus musculus chordata; Crani gukaryota; Metazoa; Chordata; Sciur Mammalia; Eutheria; Rodentia; Sciur Mammalia; 1 to 227271)

1 (bases 1 to 227271)

1 (bases 1 to Musculus clone McPherson, J.D. and Waterston)
                                                                                                                             AC122205.1 GI:21105035
                       The sequence of Mus musculus
                                                                                                      Mus musculus.
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Sciurognathi; Muridae; Murinae; Mus
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Sequencing vector: Dlasmid; 1008
Sequencing vector: Dlasmid; 1008
Chemistry: Dye-trimer ET; 08 of reads
Chemistry: Dye-terminator Big Dye; 1008 of re
Consensus quality: 217681 bases at least Q30
Consensus quality: 220647 bases at least Q20
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Direct Submission
Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 219000; agarose-fp
Insert size: 235763; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
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184792: contig of 1330 bp in 1
184892: gap of unknown length
199072: contig of 14180 bp in 1
199172: gap of unknown length
213327: contig of 14155 bp in 1
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227271: contig of 13844 bp in 1
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AC100738
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Mus musculus clone RP24-362K21,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                     Mus musculus
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6726. .8003
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33006. .35141
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23198. .25368
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11563. .12633
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10190. .11462
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12734. .13913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choepel, V. Collangelo, M. Collins, S. Collymore, A. Cook, A. Cooke, P. DeArellano, K. Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W. Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamezares, R., Landers, T., Lehocky, J., Levine, R., Liu, G., MacCearn, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., McCearthy, M., McDwan, P., McRernan, K., McPheteters, R., Meldrin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Muylor, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Noure, C., Nogov, P., Raymond, C., Retta, R., Risback, M., Riley, R., Sec, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schuer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Travis, N., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., 2 inoun, J., Zembek, L., Zimmer, A. and Zody, M. O2141, USA Subramanian, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, B., Mux, Y., Wyman, D., Ye, W.J., Young, G., 2 (Santata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Mux, M., Chang, J., McLean, C., MacGonald, P., Major, J., Matthews, C., Kanatt, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Kanatt, A., Karatas, A., Kells, C., Landers, T., Levine, R., Rise, C., Kongov, P., Phunkhang, P., Pierreira, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Phunkhang, P., Pierreira, N., Machan, S., Severy, P., Schwer, P., Marthews, C., Mordon, C., Mordon, C., Landers, T., Schupback, R., Seaman, S., Severy, P.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A.,
Barna,N., Bastien,V., Boguslavkiy,L., B
Anderson,S., Barna,N., Bastien,V., Chand,J., Chaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 20, 2002 this sequence version replaced g1:17048105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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          Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 123002 bases at least Q30
Consensus quality: 123006 bases at least Q30
Consensus quality: 123011 bases at least Q20
Insert size: 115000; agarose-fp
                                                                                                                                                                             Center project name: .L17466
Center clone name: 362_K_21
----- Summary Statistics
Sequencing vector: Plasmid: n/a;
                                                                                                                                                                                                                                                                             Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome
     Insert size: 123016; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Lander, E.
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 15.0 in Q20 bases; agarose-fp Quality coverage: 14.0 in Q20 bases; sum-of-contigs
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/clone="RP24-362K21"
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AUTHORS
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the record is upda
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Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrin, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., NayJor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talanas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassilav, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Boukhgalter, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Collymore, A., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, Fitzhugh, W., Gage, D., Galagan, Fitzhugh, W., Gage, D., Galagan, Fitzhugh, W., Gage, D., Galagan, J., Gardyna, Fitzhugh, W., Gage, D., Galagan, Fitzhugh, W., Gage, Galagan, Fitzhugh, Fitzhugh, W., Gage, D., Galagan, Fitzhugh, W., Gage, P., Gala
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overlap relationships among clones to be deduced. However, it should not be assumed that this clone
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Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                             2379: contig of 743 bp in 1

380 2479: gap of 100 bp

180 3173: contig of 694 bp in 1ε

74 3273: gap of 100 bp

74 3968: contig of 694 bp in 1ei

74 3968: contig of 694 bp in 1ei
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8047: 02-8048: 02-8048: 02-8148

4/: gap of 8874: con

6486: gap 7207:

8875 8974: 9698 9797:

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26115: cu...
6215: gap of
26935: contig of 720 p.
27035: gap of
27755: contig of 720 bp in
6 27855: gap of
100 bp
100 bp
1100 bp
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18738: contig of
1838: gap of 1
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21186: contig of 1
286: gap of 1
22004: contig of
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311: gap of
31007: contig of
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17: gap of 1
10537: contig of
                                                                33485: contig of
                                                                                     32653: contig of
                   90: gap of 
35139: contig of
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                         290: contig of 705 bp
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965: contig of
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                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
81: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
52: contig of
                                                                                                                                                                                                                                            p of 100 bp
contig of 722 bp in length
p of 100 bp
contig of 720 bp in length
                                                                                                           contig of
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21 bp in length
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21 46720: gap of 100 bp
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                                                                                                                                                                                                                                         Direct Submission
Submitted (19-JUL-2002) Human Genome of Molecular and Human Genetics, Bay Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Center project name: GZGE
                                                                                                                                                                    Center: Baylor College of Medicine
                                                                                                                                                                                                            ---- Genome Center
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                                                                                                                                                                                                                                                                                Genome Sequencing Center, Depa
cs, Baylor College of Medicine,
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*** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                    Department
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: Phrap; version 0.990329 Consensus quality: 109118 bases at least Q30 Consensus quality: 113028 bases at least Q30 Consensus quality: 116051 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-AUG-2002) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 15, 2002 this sequence version replaced gi:22205033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL845338 172121 bp DNA Mus musculus chromosome 4 clone RP24-480C2, PROGRESS ***, 8 unordered pieces.
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Insert size: 161713; 4.7% error; agarose-fp
Quality coverage: 5.08x in Q20 bases; sum-o
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Direct Submission
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Mammalia; Eutheria; Ro
1. (bases 1 to 172121)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://mrcseq.har.mrc.ac.uk
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47163 47262: gap of
47263 64639: contig of 17377 bp in length
64640 64739: gap of
64740 131541: contig of 68802 bp in length
131542 131641: gap of
131642 131893: contig of 3522 bp in length
131642 138993: contig of 3914 bp in length
138994 13903: gap of
139094 13907: contig of 3914 bp in length
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                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
                                               139094 143007: CULLLY ... 100 bp
143008 143107: gap of 100 bp
143108 148923: Contig of 5816 bp in
148924 149023: gap of 100 bp
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fragment_chain:1"
164622. .172121
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    32844 c    32754 g    52899 t
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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/clone="RP24-480C2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 226144 bases at least Q40 consensus quality: 226667 bases at least Q30 Consensus quality: 226920 bases at least Q20 Insert size: 197000; agarose-fp Insert size: 230199; sum-of-contiss Quality coverage: 17.61 in Q20 bases; sum-of-contigs Quality coverage: 12.04 in Q20 bases; sum-of-contigs
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AC124397.2
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McPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
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On Jul 21, 2002 this sequence version replaced gi:21426516
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Mammalia; Eutheria; Rodentia; Sci
1 (bases 1 to 228421)
McPherson,J.D. and Waterston,R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                             2211
2311
74702
74802
145740
145840
227902
228002
228051
228151
/db_xref="taxon:10090"
                         ∕organism≖"Mus musculus"
                                                                      Location,
                                                                                        2210: contig of 2210 bp in length
2310: gap of unknown length
74701: contig of 72391 bp in length
74801: gap of unknown length
145739: contig of 70938 bp in length
145839: gap of unknown length
227901: contig of 82062 bp in length
228001: gap of unknown length
228050: contig of 49 bp in length
228150: gap of unknown length
228150: gap of unknown length
228171: contig of 271 bp in length.
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                                                                         Qualifiers
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* NOTE: This is a 'working draft' sequence. It currently * consists of 7 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                      Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxto Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk chone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                            Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="assembly_name:Contig45"
145840. .227901
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228151. .228421
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228002. .228050
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2311. .74701
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Pred. No. 1.5e-09
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Best Local Similarity 40.9%;
Matches 189; Conservative
misc_feature
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                                                                        CTATTTTGTACTAGAGGGAGGTTATAAATTATTGTTATTGTTATATTCTATTTTACTGTT 1779
                                    TGTGGCAGCCTAAGTTGGTCTTGAACTCACTATGAAGCTAGCAATGACCTTGAGCTTCTG 1839
                                                                                                                                                                                  ATATTTCTCACTTTGGCAAAGTGGATGGAAAGTTGATCAAAATGAAAGTTATACTCAGAA 1719
                                                                                                                                                                                                                          9868 98967; gap of 100 bp
148933 149032; contig of 49965 bp in length
148933 149032; gap of 100 bp
149033 151927; contig of 2895 bp in length
151928 152027; gap of 100 bp
152028 155409; contig of 3382 bp in length
155410 155509; gap of 100 bp
155510 158708; contig of 3199 bp in length
158709 158808; gap of 100 bp
158809 180964; contig of 3199 bp in length
Location/Qualifiers
1500 180964; contig of 22156 bp in length
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87240 9886
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fragment_chain:1"
158809. 180964
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fragment_chain:1"
149033. _151927
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152028. .155409
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/clone_lib="RPCI-23"
l. .87139
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fragment_chain:1
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fragment_chain:1"
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fragment_chain:1"
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239: gap of 100 bp
98867: contig of 11628 bp in length
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Pred. No. 1.7e-09;
0; Mismatches 272;
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Search completed: February 17, 2003, 15:04:36 Job time: 7849.09 secs

Sequence 5, Appli Sequence 3, Appli Sequence 46, Appli Sequence 2047, Appli Sequence 15, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 17, Appli

Sequence

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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1 US-08-232-463-14
US-09-810-347-3
4 US-09-810-347-3
4 US-09-735-934-3
1 US-08-795-252-95
5 PCT-US96-06352-95
5 PCT-US96-06383-95
1 US-08-135-511-32
1 US-08-187-453-32
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1 US-09-244-796-3
1 US-09-244-796-3
1 US-09-244-796-32
1 US-09-34-001C-1200
1 US-09-09-033-428-2
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US-08-232-463-14
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        Query Match
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMPELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                  IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
THIE OF INTENTION: DECOMPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1800 Diac
CITY: Alexandria
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US-09-238-303-7
US-09-734-675-3
US-09-712-016-46
US-09-714-001C-2047
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US-08-335-844A-15
US-08-895-628-3
US-08-895-628-3
US-08-895-610D-3
US-08-895-810D-3
US-08-895-810D-3
US-08-895-810D-3
US-08-948-705-3
US-09-345-882-7
US-09-268-992-7
US-09-0657-477
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; ORGANISM: Human
US-09-810-347-3
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APPLICANT: YE, Jane et al.
APPLICANT: YE, JANE et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1169
CURRENT APPLICATION NUMBER: US/09/810,347
CURRENT FILING DATE: 2001-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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SOFTWARE: FastSEQ for
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                                                                                                                                                     12430 CTTCATGCCAGGAAATCAATGTGTTGTTCTCATCACTCTACTTGTTTCTTCCCACCTCCA 12489
12550 TACTTCCTCCTTTTTTTCCATCTGTCCTCATCTCTCATTTCAGAACTCTTATTAAGCC 12607
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                                  557 ATTGCTGCAAAGTCTTGAGAAGTCTAGTCTTATGGATCTCCTTTTCTCCTCAGGTCTCCT 616
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                                                                                                              GGTCTCCACACACCATTCACACTTCTTGA-----ATATTCTTTGAACATAACAAATT 668
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                                                                         GAGCATCACACATGTCACTCGCTGCAATCCCCCCAATGATATACTTCACCCATCCGACATT
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51.7%;
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Live 236; Mismatches 136;
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Pred. No. 0.057;
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RESULT 4
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SEQ ID NO 3
LENGTH: 43950
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Patent No. 5705343
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: CL00085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LI, Jiayin et al
                  TELEX:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                      REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD TO DIAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1126 TGTTTTGAGACGCCAGAAATCTGACACCAGTTTCAATGTTTAGACTTGATGCACACCTGT 1185
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                                                                                                                                                                                        FILING DATE: 0:
CLASSIFICATION:
                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20006-1888
                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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                                  90-4030
                  FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIMMEL, BRUCE E.
THOMAS, WINSTON J.
WOLEF, ROGER K.
VENTION: METHOD TO DIAGNOSE HEREDITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRAYNA, DENNIS :
FEDER, JOHN N.
GNIRKE, ANDREAS
                                                        (202) 887-0763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
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; TOPOLOGY: US-08-599-252-95

TYPE: r

1166 base pairs

TYPE: nucleic acid STRANDEDNESS: single

linear

Matches Query Match

Local Similarity les 45; Conserv

Conservative

0,

2.4%;

Score 35.4; DB Pred. No. 0.31; Mismatches

DB 1; 16;

Length 1166;

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                                                                                                                 PCT-US96-06352-95
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                                                              Query Match
Best Local
                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS
1081 TAACACAAACTTAATAGATTAAAACAGCACGGATTTATTCTCACATGTTTTGAGACGCCA 1140
                                                                                                                                                                                                                                                              RECISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1. CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
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                                                                                                                                TOPOLOGY:
                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                               TELEFAX:
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                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               NAME: MURASHIGE, KATE H.
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                                                                                                                                                                nucleic acid
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KIMMEL, BRUCE E.
THOMAS, WINSTON J.
WOLFF, ROGER K.
VENTION: METHOD TO DIAGNOSE HEREDITARY
VENTION: HEMOCHROMATOSIS
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                                                  Conservative
                                                                                                                                  linear
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                                                Score 35.4; DB Pred. No. 0.31; 0; Mismatches
                                                                               DB 5;
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US-08-135-511-32

Sequence 32, Applicat Patent No. 5558999 GENERAL INFORMATION:

Application US/08135511

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PCT-US96-06583-95/c; Sequence 95, Applica; GENERAL INFORMATION
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                                                                                                                         Matches
                                                                                                                                                      Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                         COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 90:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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TELEFAX: 90-4030
TEX: 90-4030
97 G 97
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                                                                                                                                      Local
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                                                                                                                       1 Similarity
45; Conser
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KIMMEL, BRUCE E.
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; MOLECULE TYPE: DNA (genomic)
US-08-135-511-32
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Patent No. 5650286
GENERAL INFORMATION:
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                               ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                 APPLICANT: CHIANG, John Young Ling
TITLE OF INVENTION: Genomic DNA of Human Cholesterol
TITLE OF INVENTION: 7a-Hydroxylase and Methods of Us
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TELEFAX: (202)672-5399
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MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                862 CCATG 866
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Local Similarity 55.2%;
les 69; Conservative
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                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/135,511 FILING DATE: 13-OCT-1993
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 OPERATING SYSTEM:
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3000 K Street, N.W.,
                                                                                                                                          E: Foley & Lardner
3000 K Street, N.W., Suite 500
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SYSTEM: PC-DOS/MS-DOS
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PC compatible
EM: PC-DOS/MS-DOS
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Regulatory Elements and Methods
35
                                                                                                                                                                                                                 7a-Hydroxylase and Methods of Using
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US-08-361-458-4
                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08361458
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 18/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
TETER AX: (202)672-5399
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LENGTH: 5537 base pair
CURRENT APPLICATION DATA APPLICATION NUMBER: U
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STREET: 3000
STREET: 3000
Mashington,
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                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCTTCTTCTCATTCAGATCTCAAATGTCACAATTTCAGAGAGCCCATCTCTGATCATC 1207
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                                                                                                                                                  E: Foley & Lardner 3000 K Street, N.W ashington, D.C.
                                                                                                                                                                                                                                                                       Chiang, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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13-OCT-1993
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13-OCT-1993
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                                                                                                                                                                                                                                    Genomic DNA of Human Cholesterol 7a-hydroxylase and Methods for Using it
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us/08/361,458
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                                                                                                                                                                    Suite 500
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Gaps

FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CLASSIFICATION:

US 08/135,488

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US-08-477-953-9
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 5537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                            FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,458
                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,953
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-0CT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHIANG, John Young Ling
TITLE OF INVENTION: Genomic DNA of Human Cholesterol
TITLE OF INVENTION: 7a-Hydroxylase and Methods of Using
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                               APPLICATION NUMBER: US 08/135,511 FILING DATE: 13-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
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APPLICATION NUMBER:
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 US 08/135,510
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Pred. No. 0.
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GENERAL INFORMATION:
APPLICANT: Chiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1148 TCTCTTCTTGTCATTCAGATCTCAAATGTCACAATTTCAGAGAGCCCATCTCTGATCATC 1207
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1268 ACATG 1272
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                                                            FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     APPLICATION NUMBER: US 0: FILING DATE: 13-OCT-1993
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 28-JAN-1994
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                              NAME: SANDERCOCK, COREGISTRATION NUMBER:
                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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3000 K Street, N.W., Suite 500
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13-OCT-1993
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Regulatory Elements and Transcription Factors
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                                               Colin G
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INFORMATION FOR SEQ ID NO:

32:

90413

TELEFAX:

: (202)672-5300 (202)672-5399

SEQUENCE CHARACTERISTICS:

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US-08-562-985A-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: CHIANG
                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5537 base pairs
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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TELEFAX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5537 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                               STRANDEDNESS: single
                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/562,985A FILING DATE: 27-NOV-1995
NAME/KEY:
LOCATION:
                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                 nucleic acid
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                        (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STROUP, Diane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHIANG, John Y.L.
                CDS
join(2300..2380, 3930..4169, 5211..5537)
                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AN ASSAY FOR AGENTS THAT AFFECT CHOLESTEROL 7ALPHA-HYDROXYLASE EXPRESSION AND A CHARACTERIZATION OF ITS REGULATORY ELEMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.4%;
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-477-952-9
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US-08-477-952-9
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Best Local Similarity
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                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 18748/221 HOCE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/135,488 FILING DATE: 13-OCT-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 1
FILING DATE: 21-DEC-
PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                              FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/135,510 FILING DATE: 13-OCT-1993
                                                                                                                      LENGTH:
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DEDNESS: single
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                                                                        linear
                                                 DNA (genomic)
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Genomic DNA of Human Cholesterol
7a-Hydroxylase and Methods of Using It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.2%;
2.4%; Score 35.4;
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 DB
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Length 5537;
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Query Match

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; SEQ ID NO 3; LENGTH: 8758; TYPE: DNA; ORGANISM: Human US-09-799-345-3
                                   ; SEQ ID NO 10
; LENGTH: 1339
; TYPE: DNA
; ORGANISM: MUTINE
US-09-442-143A-10
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US-09-799-345-3/c
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; Sequence 10, Application US/09442143A
; Patent No. 6403089
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APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLAT
TITLE OF INVENTION: ACID M
TITLE OF INVENTION: THEREO
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Best Local Similarity 63.5%;
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
Query Match
                                                                                                                                                                  APPLICANT: Levy, Gary
APPLICANT: Clark, David A.
APPLICANT: Clark, David A.
TITLE.OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442,143A
CURRENT FILING DATE: 1997-11-15
PRIOR APPLICATION NUMBER: US 60/046,537
PRIOR APPLICATION NUMBER: US 60/061,684
PRIOR FILING DATE: 1997-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
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CURRENT FILING DATE: 2001-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                             NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THEREOF
   2.28;
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0; Mismatches
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Pred. No. 1.1;
0; Mismatches 31;
   Score 33.6;
   DB 4;
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   Length 1339;
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Search completed: February 17, 2003, 16:11:05 Job time: 125.486 secs

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: gb_ba:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	cor 94.	9 tc	eng	DB 2	12514	SCI
ω ω ⊢	274	49.5	219386 187332 165503	งผม	112	מֿמֿנ
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	57.2		625	ν,	C0158	015
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	2	5	981	9	3595.	359
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13	0		7288	N	1135	113
14	0	.4	932(	N	179	117
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ي د	١.		6875	N	06896	5890
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43	•	ľ	6124	^		1
443	47.2	٠.	6124 5681	9 1	SJ631M13	ALI1733

## ALIGNMENTS

DNA	
Mus musculus chromosome UNK clone RP24-350A15, WORKING DRAFT	
SEQUENCE, 8 unordered pieces.	
AC125147	
AC125147.2 GI:21539180	
HTG; HTGS_PHASE1; HTGS_DRAFT.	
house mouse.	
Mus musculus .	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus	
1 (bases 1 to 219386)	
McPherson, J.D. and Waterston, R.H.	
The sequence of Mus musculus clone	
	AC125147  AC1251

Pred.

No. is the number of results predicted by chance to have a

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FEATURES
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AUTHORS
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                                                                     misc_feature
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misc_feature
                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Mi3; 0%
Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 216121 bases at least 040
Consensus quality: 216506 bases at least 030
Consensus quality: 216719 bases at least 020
Insert size: 171000; agarose-fp
Insert size: 217980; sum-of-contigs
Quality coverage: 14.92 in 020 bases; sgarose-fp
Quality coverage: 11.97 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished 2 (bases 1 to McPherson, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (20-JUN-2002) Genome Sequencing Center, 4444
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 219386)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-JUN-2002) Genome Sequencing Center, Parkway, St. Louis, MO 63108, USA On Jun 22, 2002 this sequence version replaced gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: M_BB0350A15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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80946
138243
138343
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807
907
5270
5370
16394
16494
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34652
34752
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907. .
                                  /note="assembly_name:Contig19"
5370. .16393
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 /note="assembly_name:Contig20"
16494. .34651
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1. .219386
                                                                                                                                                                          /db_xref="taxon:10090"
/chromosome="UNK"
                                                                                                                                                        /clone="RP24-350A15"
                                                                                                                                                                                                           organism="Mus musculus"
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138242: contig of 57297 bp in
138342: gap of unknown length
219386: contig of 81044 bp in
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34651: contig 0
34751: gap of 0
80845: contig 0
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                                                                                                                   assembly_name:Contig12"
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205:
806:
906:
                                                                                  assembly_name:Contig14"
                                                                                                                                                                                                                                                /Qualifiers
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contig of 4363 bp in length
gap of unknown length
contig of 11024 bp in length
gap of unknown length
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Best Local Similarity
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 119540 GTCTGCTGCCACCACCATGACCATCCCCATGAATACAGACACTGCCTTCTTAGTGTT
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                                                                                                           GGCTCTCCAAGAGAATAATTTGAAAAGCATTTTGCTATTCTATCAAGTGATCATACAAT
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                                                                                                                                                                                                                                                                                              CTCAGGTCTCCTGGTCTCCACACACCATTCACACTTCTTGAATATTCTTTGAACATAACA 119359
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Direct Submission
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                                                                      Eukaryota; Metazoa;
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 Adio-Oduola, B.,
                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
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SEQUENCING IN PROGRESS
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; Murinae;
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COMMENT

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
NOTE: This is a 'working draft' sequence. It currently

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:18701283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-FEB-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 85091 bases at least Q40 Consensus quality: 91433 bases at least Q30 Consensus quality: 97328 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                         Center project name: GMMD Center clone name: CH230-142F15 ---- Summary Statistics Sequencing vector: Plasmid;
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consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality above 40 are expected to have less than
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Bummalla; Eutheria; Primates; Catarrhini; Hominidae;
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All manually edited bases have been reduced to qual Quality levels above 40 are expected to have less to 1 error in 10,000 bp.
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Submitted (06-AUG-2002) Production Sequencing Facility, DC Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94 on Aug 6, 2002 this sequence version replaced gi:18139346.
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                                                      GGTATCTTCATGACATCTCGAATATTTCCAATTTCTCTATTGCTGCAAAGTCTTGAGAAG
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166494
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter
                                                                                                                                                                                                                                                                                                                                                                            Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified.
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1491 c 1486 g
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGTACCAAATTCTTCTATCTCTTTAA 1459
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Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 26, 2000 this sequence version replaced gi:6446837. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L.,
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AC015831.2 GI:7329398
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Homo sapiens clone RP11-688G24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens, clone RP11-688G24
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                              overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                    NOTE: This record contains 173 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                           be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center Center code: WIBR Web site: http://www-seq.wl.mit.edu
858: contig of 858 bp
958: gap of 100 bp
1834: contig of 876 bp
1934: gap of 100 bp
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8710 9573: contig of 8, 9574 9673; gap of 1037 contig of 8, 10537; gap of 10, 10638 10637; gap of 10, 10638 10637; gap of 10, 10638 10637; gap of 10, 10638 10621; gap of 10, 10622 11621; gap of 10, 10646; contig of 8, 10646; contig of 8, 10646; gap of 10, 10646; g
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14520 15368:
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28 27991: contig of 8

29 27891: gap of 10

29 28742: contig of 8

42 28842: gap of 10

43 28842: gap of 10

29689: gap of 10

20642: contig of 8

30 29789: contig of 8
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2 18185: contig of 8
2 18185: gap of 10
16 18285: gap of 10
17 19098: contig of 6
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6 23957: contig of 8
8 24057: gap of 10
8 24926: contig of 8
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7684:
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9 19198: qap
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3789:
  36555: gap of 
37414: con
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34521: contig of
34621: gap of 1
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35483: ci
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31640: contig of
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33554: contig of
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32602: contig of
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26827: contig of
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36455: contig of
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25881: contig of
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On Sel
                                                                                                                                 Direct Submission
Submitted (29-SEP-2001) Multimegabase Sequencing Center, for Systems Biology, 4225 Roosevelt Way NE, Suite 200, St
                                                                                                                                                                                                                                                              Submitted (08-MAR-2000) Multimegabase Sequencing Center, of Washington, PO BOX 357730, Seattle, WA 98195, USA 3 (bases 1 to 128484)
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                                                                                                                                                                                                Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                          Center code: UWMSC
                                                         Center: Multimegabase Sequencing
Contact: leerowen@systemsbiology.org
                     Web site: http://chroma.mbt.washington.edu/msg_www
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eattle, WA
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Best Local Similarity 48.5
Matches 149; Conservative
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Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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87236. 128484
/note="overlap with RP11-292P13,
105444. 105452
/note="low quality data"
127261 c 26033 g 36526 t
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/note="This clone overlaps RP11-15117 AC009996 and
RP11-292P13 AC018901. Data from overlapping BACs wa
added and the consensus sequence determined from
CTD-2165P21 to the extent possible."
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/chromosome="15"
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Location/Qualifiers
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51502. .51594
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Pred. No. 0:0032;
0; Mismatches 16
                                                                                        162495 bp
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15 clone RP11-151N17 map 15q15,
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Best Local Similarity 48.1
Matches 149; Conservative
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Submitted (28-ApR-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
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On Apr 28, 2001 this sequence version replaced gi:13621216.
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(bases 1 to 162495)
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Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: leerowen@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://chroma.mbt.washington.edu/msg_www
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/note="Data from overlapping BACs CTD-2329K10, CTD-2154L5
and CTD-2165P21 were added and the consensus sequence was
determined from RP11-151N17 to the extent possible."
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126759. .126851
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                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL: SW:
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 LSA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Con Feb 1, 2002 this sequence version replaced gi:18250465.
IMPORTANT: This sequence is not the entire insert of clone RP11-9801 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                           SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
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AL359543
                                                                                                                                                Group Further information can be found http://www.sanger.ac.uk/HGP/Chr1 http://www.sanger.ac.uk/HGP/Chr1 11.1 c RP11-9801 is from the library RPCI-11.1 c Pieter de Jong For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brown, A
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                                                                                                                        nttp://www.chori.org/bacpac/home.htm
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Bastlen, V., Boguslavkly, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collims, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (S Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Direct, S. Shwission, Simmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 178985)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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AC015524.7
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                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/chromosome="1"
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on May 1, 2001 this sequence version replaced gi:12621436.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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----- Project Information
Center project name: L4275
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1772. 310
                                                                                                                                                                                                                                                                                                                    /rpt_family="L3" 6936. .7231
                                                                                    complement(9071. .9445)
/rpt_family="Charlie2"
complement(9447. .9737)
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7232. .7313
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/rpt_family="L3"
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complement(12026. .12454)
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/db_xref="taxon:9606"
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/rpt_family="MLT1H"
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29246
                                                                                                                                                                                                                                          /rpt_
29141
                                                                                                                                                                                                                                                                                                                                                /rpt_
28538
                                                                                                                                                                                                                                                                                                                                                                                                                     complement(27694. .27765)
/rpt_family="MIR"
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26761
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24802. .24857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(TA)n"
24013. .24430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(22330. .22471)
/rpt_family="MIR"
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/rpt_family="MER102b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AT_rich"
complement(16513. .16856)
/rpt_family="MLT1A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Tigger2a"
13283. .13344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(19595. .19782)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MLT1H1"
        rpt_family="(TA)n"
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3. ,20%%
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                                                                                                          family-"AluJb"
                                                                                                                                                          tamily-"L1MA9"
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AUTHORS
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SOURCE
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AC021757/c
        COMMENT
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                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Bedaif, A., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Bedaif, A., Costle, A., Cohepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Naylor, J., Naylor, J., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, McKernan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fitzeria and McKernan, McKernan
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Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 24, 2001 this sequence version replaced gi:13259440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 201156)
Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, Ohono sapiens, clone RP11-45M11 Unpublished
                                                                                                        Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
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                                                                                  Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201156)
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AC021757.5 GI:14192966
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complement(30333...30650)
/rpt_family="L1PA8"
31149...3140
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complement(31488. .31779)
/rpt_family="AluJb"
31780. .31917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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HTG 24-MAY-2001

7 unordered

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BASE COUNT
ORIGIN
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Query Match
Best Local Similarity
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Consensus quality: 196395 bases at least Q40

Consensus quality: 198941 bases at least Q30

Consensus quality: 198947 bases at least Q30

Consensus quality: 19997 bases at least Q20

Insert size: 200000; agarose-fp

Insert size: 2000005; sum-of-contigs

Quality coverage: 5.8 in Q20 bases; agarose-fp

Quality coverage: 5.7 in Q20 bas.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                   64954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50677 116260
116267 116366:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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19582 19681: gap of 100 bp
19682 25463: contig of 5781 bp in length
25463 25562: gap of 100 bp
                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
50677. .116266
                                                                                                                                                 clone_end:T7
                                                                                                                                                                                                   /note="assembly_fragment"
32045. .50576
                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment" 25563. .31944
                                                                                                                                                                                                                                                       116367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="RP11-45M11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                         note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19682.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11 Human Male BAC"
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                                                                                             ector_side:right"
35473 c 37723 g 62403 t
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3.4%;
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contig of 42012 bp in length
Score 51.4; DB 2; Pred. No. 0.0082;
                                                                                                                                                                                                                        y_fragment"
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Philos, R., Santos, Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Stojanovic, N., Subramanian, A., Wheeler, J., Wu, X., Stojanovic, N., Stoj
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 167746)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblag-Toh, K., Liu, G., MacChean, C., MacConald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Minga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, Norbu, C., Norman, C.H., O'Coonor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
                                                                                                                                                                                                                                                                                                                                 Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE

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Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrin, J., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Neldrin, J., Mathews, C., McCarthy, M., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Staman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Wynan, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimper, A., and Zody, M.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Clang, J.,
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Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Tarvino, R., Illey, I.,
Tarvino, R., Ill
                                                                                                                                                                                                                                                                                                                             Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 30, 2002 this sequence version replaced gi:20219178. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RN/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson, R., Jones, C., Kamat, A., Karatas, A., Keils, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levlne, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stanger, R., Seaman, R., Stanger,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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    Center project name: L2118 Center clone name: 171_G_:
                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submission
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6744. .6839
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complement(5457. .5756\
/rpt_family="""
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14222. .14301
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/rpt_family="MIR"
13268...13702
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complement(12483. 12487)
/note="<30 qual. SNGL region"
complement(12532. 12542)
/note="<30 qual. SNGL region"
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/note="<30 qual. SNGL r
complement(7204..7503)
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10780
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complement(4776. .4
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3552. .3812
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complement(393. .688)
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9822. 1010'
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complement/7107
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117. 5167
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/db_xref="taxon:9606"
rpt_family="MER33"
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                                                                                           _family="AluJo"
                                                                                                                                                                                                                                                                                  _family="MER5B"
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                                                                                                                                                                                  family="MER33"
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les 63; Conserv
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Binkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, O.L., Maduro, V.B., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, Pearson, R., Prasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-MAR-2002) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA
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AC113567.1 GI:19071598
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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    (bases 1 to 172884)

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                 Center project name: cio
Center clone name: 265M12
Center clone name: 265M12
Center clone name: 265M12
Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 172016 bases at least 040
Consensus quality: 172086 bases at least 030
Consensus quality: 172156 bases at least 020
Insert size: 134000; agarose-fp
Insert size: 172784; sum-of-contigs
Quality coverage: 9.59x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                              Comparative Sequencing Initiative
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/rpt_family="AluY"
complement(17815..17922)
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                                                                                                                                                                                                                                    Submitted (11-APR-2002) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                           Center: NIH Intramural Sequencing Center code: NISC
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/db_xref="taxon:9615"
/clone="RP81-265M12"
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69.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
Muzny, D., Arenson, A.D., Brundage, E., Carvelli, K., Chen, E., Di, V
Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C.,
Goodman, M., Gorrell, J. H., Haywood, M., Jackson, L., Kampal, R.,
Karpathy, S., Leal, B., Liu, W., Logan, O., Lu, J., Ly, T., Martinez,
Oswal, G., Perez, L., Rashid, N.D., Rowland, K., Savage, L.,
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                    Homo sapiens Xp22 PAC
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                                                                                                                                                                                                                                                                  AC003667.2
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                                                                                                                  (bases 1 to 134019)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 154000; agarose-fp
Insert size: 193109; sum-of-contigs
Quality coverage: 11.42x in Q20 bases; agarose-fp
Quality coverage: 9.11x in Q20 bases; sum-of-contigs
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/clone="RP81-37219"
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on Feb 26, 2002 this sequence version replaced gi:2995482.
On Feb 26, 2002 this sequence version replaced gi:2995482.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-APR-1998) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA 6 (bases 1 to 134019)

Morley.K.C.
Direct Submission
Submitted (26-FEB-2002) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-MAR-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Submitted (09-DEC-1997) Molecular and Human Genetics, Bay
College of Medicine, One Baylor Plaza, Houston, TX 77030,
                                                                                                                                                                                                                                                                                                                                                                                             were canonical splice junctions across the splice junctions.
                                                                                                                                                                                                                                                                                                                                                                                                                   Exon/Intron boundaries of identified were canonical splice junctions that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence similarities were identified using Powerblast by Jinghui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The repeat regions shown were identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-MAR-2002) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, US
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Direct Submission
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Direct Submission
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86.
                                                                                                                                                                                     /clone_lib="Research Park Cancer Institute PAC library"
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                                                                                                                  complement(1. .2004)
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                                                                  'function="clone overlap"
                                                                                          'note="overlaps bases 1.
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                                                                                             .2004 of clone AC112916'
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complement(6158...6737)
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lomo sapiens"
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Search completed: February 17, 2003, 14:17:04 Job time: 5503.95 secs
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35217. .3551%
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27242 . 27373
/standard_name="A002D07, Chr. -,
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compigment(28252 . 28361)
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/rpt_family="L1M4"
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Listing first 45 summaries
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                         1111
      AAK05289;
                                                                                                                                                                             1051
                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                              AAK05289 standard; DNA;
                                                                                                                                                                                                                                                      Sequence 472 BP; 101 A; 102 C; 101 G; 168 T; 0 other;
                                                                                                                                                                                                                                                                                printed specification,
from WIPO at ftp.wipo.i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
                                                                                                                                                    164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA57262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA57262 standard;
                                                                                                               GGATTTATTCTCACATGTTTTGAGACGCCAGAAATCTGA 1149
                                                                                                                                                                   GTCCATGCTGGTTTCCGTATTGATTGTTTCTAACAACTTAATAGATTAAAACAGCAC 1110
                                                                                             AAATTTATTCTCTCACAGTTCTAGAGGCCAGAAATCTGA 262
                                                                                                                                                GTACTGGATTTTTCAAGGCTTCTGTGAGATTACCACAAACTTGGTGGCTTAAAACAACAG 223
                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the ed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                         genome-derived single exon nucleic acid probes useful
zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           foetal
                                                                                                                                                                                                      65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                               ID NO 5567; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0236359
2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                               3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression; single exon nucleic acid probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                              472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                              ВP
                                                                                                                                                                                                    Score 44.6; D
Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR;
                                                                                                                                                                                                  DB 22;
).0035;
hes 34;
                                                                                                                                                                                                                            Length
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #5567
                                                                                                                                                                                                                             472;
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                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                        1111
 Homo sapiens
                          microarray;
                                     Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                Human bone marrow expressed single exon
                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                           1051
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                      AAK30881;
                                                                                                                                               AAK30881 standard;
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray; Alzheimer's epilepsy; cancer; ss.
                                                                                                                                                                                                               224
                                                                                                                                                                                                                                                                  164
                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; brain expressed exon; gene
microarray; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-2001
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                     GGATTTATTCTCACATGTTTTGAGACGCCAGAAATCTGA 1149
                                                                                                                                                                                                                                                                                       GTCCATGCTGGTTTCCGTATTGATTGTTTCTAACACAAACTTAATAGATTAAAACAGCAC 1110
                                                                                                                                                                                                              AAATTTATTCTCTCACAGTTCTAGAGGCCAGAAATCTGA
                                                                                                                                                                                                                                                                GTACTGGATTTTTCAAGGCTTCTGTGAGATTACCACAAACTTGGTGGCTTAAAACAACAG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      brain expressed single exon probe
                                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon nucleic acid probes for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                     472 BP; 101 A; 102 C; 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                           cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO:
                                                                                                                                               DNA;
                        leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                               3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                472
                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650pp +
                                                                                                                                                                                                                                                                                                                Score 44.6; DB 22;
Pred. No. 0.0035;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression analysis;
ase; multiple sclerosis; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank
                                                                                                                                                                                                                                                                                                                                                                     G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                     168 T;
                                                                probe SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                    DB 22;
                          myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ħ
                                                                                                                                                                                                              262
                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO:
                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5280
                                                                NO: 5438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe;
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Best Local S
Matches 65
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acprobes which are derived from genomic sequences expressed in the bone marrow. They can be used to measure gene expression in bone a samples, which may enable the improved diagnosis and treatment of such as lymphoma, leukaemia and myeloma. The present sequence is the probes of the invention.
                                                                                                                                                                                                                                                                 1051
                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn
                                        30-JAN-2001;
                                                        09-AUG-2001.
                                                                       WO200157272-A2
                                                                                                                                            17-OCT-2001
                                                                                                                                                                            AAI36794 standard;
                                                                                                                                                                                                                                                                                                                                                                                   Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157276-A2
                                                                                                                                                                                                                                                 164
                                                                                                                                                                                                                  224
                                                                                     sapiens
                                                                                                                                                                                                                                              GTACTGGATTTTCAAGGCTTCTGTGAGATTACCACAAACTTGGTGGCTTAAAACAACAG
                                                                                                                                                                                                                                                                GTCCATGCTGGTTTCCGTATTGATTGTTTCTAACACAAACTTAATAGATTAAAACAGCAC 1110
                                                                                                                                                                                                                                 GGATTTATTCTCACATGTTTTGAGACGCCAGAAATCTGA 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                          SG,
                                                                                                                                                                                                                  AAATTTATTCTCTCACAGTTCTAGAGGCCAGAAATCTGA
                                                                                                                             #5480
                                                                                                            microarray; human;
                                                                                                                                                                                                                                                                               l Similarity
65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS
                                                                                                     disorder;
                                                                                                                                                                                                                                                                                                                472
                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel
                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                             used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-023659.
2000US-023659.
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                               BP;
                                                                                                                                            (first
                                       2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001WO-US00668.
                                                                                                                                                                                                                                                                                                                                                                                    ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   expression
                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                          DK,
                                                                                                                             δ
                                                                                                                                                                           DNA;
                                                                                                                            measure
                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                               Α;
                                                                                                                                                                                                                                                                                       3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen
                                                                                                                                                                                                                                                                                                                                                                                  5438; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                102
                                                                                                                                                                            472
                                                                                                            placenta; antenatal
                                                                                                                                                                                                                                                                                                                                                                                                   in
                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ,
                                                                                                                            gene
                                                                                                                                                                                                                                                                               Score 44.6; D
Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                               ũ
                                                                                                                                                                           В₽
                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
                                                                                                                             expression
                                                                                                                                                                                                                                                                                                                                                                                                   bone
                                                                                                                                                                                                                                                                                                              G;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DR;
                                                                                                                                                                                                                                                                                                              168 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                   marrow
                                                                                                                                                                                                                                                                                        .0035;
                                                                                                                                                                                                                                                                                                DB
                                                                                                                             ä
                                                                                                                                                                                                                                                                                             1 22;
                                                                                                                                                                                                                                                                                34;
                                                                                                             diagnosis;
                                                                                                                            human placenta sample
                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                          nucleic acu
                                                                                                                                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                               472;
                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                    cancers
                                                                                                                                                                                                                                                                                                                                                     marrow
                                                                                                                                                                                                                                                 223
                                                                                                                                                                                                                                                                                0;
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RESULT 6
ABS05629
Matches
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Best Local
                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                               chronic obstructive pulmonary disease; interstitial lung dis
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1051 GTCCATGCTGGTTTCCGTATTGATTGTTTCTAACACAAACTTAATAGATTAAAACAGCAC 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microcarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                             Homo
                                                                                                                                                                                                                               pulmonary histiocytosis; lymphangioleiomyomtosis; Kar
pulmonary alveolar proteinosis; fibrocystic pulmonary
primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing
                                                                                                                                                                                                                                                                                                                                                                     19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
(MOLE-)
                                                                                                                     30-JAN-2001;
                                                                                                                                              15-NOV-2001
                                                                                                                                                                      WO200186003-A2
                                                                                                                                                                                                                     nyarine
                                                                                                                                                                                                                                                                   Hermansky-Pudlak syndrome; sarcoidosis; pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                   ABS05629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164
                                                                                                                                                                                             sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATTTATTCTCACATGTTTTGAGACGCCAGAAATCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACTGGATTTTTCAAGGCTTCTGTGAGATTACCACAAACTTGGTGGCTTAAAACAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-488897
                                                                                                                                                                                                                                                                                                                                          genome-derived single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome-derived
                                                                                                                                                                                                                                                                                                                   ds; single exon probe; asthma; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Conserv
 MOLECULAR DYNAMICS
                                                                                                                                                                                                                     membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472
                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID No 5480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel
                      2000US-180312P.
2000US-207456P.
2000US-0609408.
2000US-0632366.
2000US-034687P.
2000US-234687P.
2000US-236359P.
2000US-236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                      2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erived single expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 A; 102 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DK,
                                                                                                                                                                                                                     disease.
                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    472
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 INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                           probe from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.6; DB 2
No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 168 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
nta -
                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                           lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes useful
                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                                                                                                           Karagener syndrome;
nary dysplasia;
                                                                                                                                                                                                                                                                   haemosiderosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                   COPD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472;
                                                                                                                                                                                                                                                                                                         disease;
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ABA63327
ID ABA(
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DT 01-1
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                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC probes: Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a calculeic acid expressed in the human lung; measuring gene expression in a cC sample derived from human lung, comprising (a) contacting the array with CC acids derived from human lung, comprising (a) contacting the array with CC mRNA, and (b) measuring the label detectably benome, comprising (c) contacting the array with CC (a) algorithmically predicting at least one exon from genomic sequences CC of the eukaryote; and (b) detecting specific hybridisation of detectably CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, CC having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, CC comprising (a) identifying exons from genomic sequence by the method can be added to the expression of the exons in the tissues and/or cell types using hybridisation to a single exon comprising one captures having a probe with the exon, where a common pattern of CC expression and for identifying exons in a gene; a peptide comprising one conditions of the exons should be assigned to a single gene; a peptide comprising one captures manalysis, and for identifying exons in a gene, particularly cusing human lung derived mRNA and for the study of lung diseases (CC pD), interstitial lung disease (ILD), familial idiopathic pulmonary disease (CC plumonary disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary collarsy dyshrinesis, pulmonary hypertension con the invention. The probes are a single exon can hypaline membrane disease. The present sequence is a single exon conditionary dysplasta, primary ciliarly dyskinesis, pulmonary hypertension of the printed specification, but was obtained in electronic.
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 65
  01-FEB-2002
                                                                                                                                                                                                                                                                                     1051 GTCCATGCTGGTTTCCGTATTGATTGTTTCTAACACAAACTTAATAGATTAAAACAGCAC 1110
                                        ABA63327
                                                                              ABA63327
                                                                                                                                                                                                             1111 GGATTTATTCTCACATGTTTTGAGACGCCAGAAATCTGA 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the printed specification, but was obtained in format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                         164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spatially-addressable
                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                          224 AAATTTATTCTCTCACAGTTCTAGAGGCCAGAAATCTGA
                                                                                                                                                                                                                                                 GTACTGGATTTTTCAAGGCTTCTGTGAGATTACCACAAACTTGGTGGCTTAAAACAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-114183/15
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                                                                                                                                                                                                                                                                                                                                   . Similarity
65; Conser
                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID No 5620; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          BP; 101 A; 102 C; 101 G; 168 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DK,
                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                   3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         set of single exon nucleic acid probes, used to on in human lung samples -
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                                                                              ВР
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                                                                                                                                                                                                                                                                                                                                           Score 44.6; Ub 2
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                                                                                                                                                                                                                                                                                                                                                                    DB 24;
                                                                                                                                                                          262
                                                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                                                                    Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        electronic
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RESULT 8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                        Human; neuregulin-1 associated gene
                                                                                                                                                                                                                                             1111 GGATTTATTCTCACATGTTTTGAGACGCCAGAAATCTGA 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                   Human
                                                                                                           17-DEC-2001
                                                                                                                                    AAK95240;
                                                                                                                                                           AAK95240 standard;
                                                                                                                                                                                                                                                                                              1051 GTCCATGCTGGTTTCCGTATTGATTGTTTCTAACACAAACTTAATAGATTAAAACAGCAC 1110
                                                                                                                                                                                                                                                                                                                                                                       Sequence 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                        119
                                                                                                                                                                                                                        179
                                                                                                                                                                                                                     AAATTTATTCTCTCACAGTTCTAGAGGCCAGAAATCTGA 217
                                                                                                                                                                                                                                                                     GTACTGGATTTTTCAAGGCTTCTGTGAGATTACCACAAACTTGGTGGCTTAAAACAACAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG
                                                                                  neuregulin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   foetal liver single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 11632; 639pp + sequence listing;
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                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                      BP; 125 A; 118 C; 127 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US00669
                                                                                                                                                           DNA; 1503900
                                                                                                                                                                                                                                                                                                                                  3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                  Score 44.6; DB:
Pred. No. 0.0039;
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                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                        1; NRG1AG1; Schizophrenia gene;
                                                                                                                                                                                                                                                                                                                                                                      209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probe #11632
                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                             579;
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RESULT 9
AAK96733
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XEXEXEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC (NRGIAGI) of the invention. The invention also relates to fragments or the invention. The invention also relates to fragments or comman Schizophrenia gene. The invention also relates to fragments or the gene and the NRGIAGI polypeptides they encode. The CC variants of the gene and the NRGIAGI polypeptides may be used in the prevention, and treatment of diseases associated with inappropriate NRGIAGI CC diagnosis and treatment of diseases associated with inappropriate NRGIAGI CC with decreased expression by rectifying mutations or deletions in a CC patient's genome that affect the activity of NRGIAGI by expressing CC inactive proteins or to supplement the patients own production of CC NRGIAGI. Additionally, the gene may be used to produce NRGIAGI and CC culturing the cell to express the protein. The gene may also be used as CC DNA probes and primers in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which CC patients may be in need of restorative therapy. The NRGIAGI polypeptides CC NRGIAGI and in assays to identify modulators of NRGIAGI expression and CC activity. Anti-NRGIAGI antibodies may also be used as diagnostic agents for detecting the presence of NRGIAGI collapse the collapse of NRGIAGI is associated with schizophrenia which conserve the detection of antibodies may also be used as diagnostic agents for detecting the presence of NRGIAGI collapse of NRGIAGI is associated with schizophrenia which conserve the detection of antibodies may also be used as diagnostic agents for detecting the presence of NRGIAGI collapse of NRGIAGI is associated with schizophrenia which conserve the collapse of NRGIAGI is associated by the above methods.
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                          51356
                                                                                                                                                                                                                                                                    1141
                                                                                                                                                                                                                                                                                                                           1081 TAACACAAACTTAATAGATTAAAACAGCACGGATTTATTCTCACATGTTTTGAGACGCCA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAG67900, AAG67901, AAG67902, AAG67903, AAAG679106, AAG67910, AAG679108, AAG67909, AAG67910, AAG679114, AAG67915, AAG67913, AAG67914, AAG67915, AAG67913, AAG67914, AAG67922, AAG67923, AAG67924, AAG67927, AAG67928, AAG67929, AAG67920, AAG67931, AAG67934, AAG67935, AAG67936, AAG67937.
               Human neuregulin-1
                                                                                                                                 AAK96733 standard; DNA; 1503900
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                                                         17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2001; 2001WO-US06376
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                                                                                                                                                                                                                                                    GAAATCTGACACCAGTTTCAATGTTTAGAC 1170
                                                                                                                                                                                                                                                                                                      TACCACCAATTTGGTGGCTTAAAACAGCAGAAATTTATGCTCTCACAGTTCTGGAGGCCA 51415
                                                                                                                                                                                                                              GAAATCAGAAATTGGTATCACTGGTGACAC 51445
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                                                                                                                                                                                                                                                                                                                                                                                 . Similarity 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1503900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 90-501; 750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associated gene 1 nucleic acids and iagnosing and treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0515715
                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosed and/or treated by the
                 gene
                                                                                                                                                                                                                                                                                                                                                                                                   2.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             452487
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                                                                                                                                                                                                                                                                                                                                                                                 Score 43.6; DE Pred. No. 0.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           281874 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gulcher JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           288074 G; 480092
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                   29;
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AAG67918,
AAG67925,
AAG67932,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragments,
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1503900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                above
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111, AAG67912,
118, AAG67919,
125, AAG67926,
132, AAG67933,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           T; 1373
                                                                                                                                                                                                                                                                                                                                                                                 0;
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밁 Ω В γ

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RESULT 10 ABA60114/c

ABA60114

standard;

DNA;

ABA60114;

01-FEB-2002

(first entry)

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This sequence represents the human neuregulin 1 gene of the invention. CC The invention also relates to fragments or variants of the neuregulin 1 cg gene. The gene and its proteins may be used in the prevention, diagnosis CC and treatment of diseases associated with inappropriate neuregulin 1 cexpression, such as schizophrenia. For example they may be used to treat disorders associated with decreased neuregulin 1 expression by rectifying cc mutations or deletions in a patient's genome that affect the activity of cneuregulin 1 by expressing inactive proteins or to supplement the patients own production of polypeptides. Additionally, the gene may be used to produce the neuregulin 1 protein, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The gene and its complementary sequences may also be used as DNA probes in claim of activity sequences may also be used as DNA probes in need of crestorative therapy. The protein may also be used as antigens in the ccl conduction of antibodies against neuregulin 1 and in assays to identify composities may also be used as antigens in the ccl candidators of neuregulin 1 expression and activity. The antibodies and composities and activity. The antibodies and activity composities and activity.
                                                                                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                          Matches
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51416 GAAATCAGAAATTGGTATCACTGGTGACAC
                                                                                                                            51356 TACCACCAATTTGGTGGCTTAAAACAGCAGAATTTATGCTCTCACAGTTCTGGAGGCCA 51415
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                                                            1141 GAAATCTGACACCAGTTTCAATGTTTAGAC
                                                                                                                                                                                                      1081 TAACACAAACTTAATAGATTAAAAACAGCACGGATTTATTCTCACATGTTTTGAGACGCCCA 1140
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1503900 BP; 452487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG67974, AAG67975
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                                                                                                                                                                                                                                                                                                      Poca T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 nucleic acids and proteins useful and treating schizophrenia -
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 345-756; 756pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG67939, AAG67940,
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                                                                                                                                                                                                                                                                          0,
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                                                                                                                                                                                                                                                                   Pred. No. 0.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                      Score 43.6; D
Pred. No. 0.7;
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   51445
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AAG67967,
AAG67973,
                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                 1503900;
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RESULT 11
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Best Local
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                              Human; gene expression; h cardiovascular disease; h congenital heart disease;
                                                                                                                                                                                                                                                                                                                       probe of the invention.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                       Probe #6940
                                                                                           23-JAN-2002
                                                                                                               ABA28474;
                                                                                                                                                                                               1141 GAAATCTGACACCAGTTTCA 1160
                                                                                                                                 ABA28474 standard;
                                                                                                                                                                                                                                           1081 TAACACAAACTTAATAGATTAAAACAGCACGGATTTATTCTCACATGTTTTGAGACGCCA 1140
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                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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30-JUN-2000;
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                                                                                                                                                                                    418
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                                                                                                                                                                                   GAAGTCTGAAATCAGTAACA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful
zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         foetal liver single
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57; Conser
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                                                                                                                                                                                                                                                                                                         585 BP; 195 A; 110 C; 131 G;
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                                                                      for
                                                                                                                                                                                                                                                                 Conservative
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2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                          (first entry)
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2000US-0608408.
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                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                           2.9%;
71.2%;
                                                                     expression analysis in human heart
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                                                                                                                                 585
                               hypertension; e; ss.
                                      heart; microarray; vascular system; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                               Score 43.2; D
Pred. No. 0.01
0; Mismatches
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                                                                                                                                                                                                                                                                                                        149 T;
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                                                                                                                                                                                                                                                                                                         0 other;
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RESULT 12
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1081
epilepsy; cancer; ss.
                               Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems. Cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                      Human brain expressed single exon probe SEQ ID NO:
                                                                                                                                                                                    05-NOV-2001
                                                                                                                                                                                                                                               AAK08390;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                          standard;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-06323687.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                          DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                         8381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
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Homo sapiens. WO200157275-A2 09-AUG-2001.

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ARKS4UZ7 13
AAKS4UZ7 16
AAKS4
XX AAKS4
AC AAKS4
AC AAKS4
XX DT O6-NC
XX Human
XX Human
XX Human
XX Homo
OS Homo
OS Homo
PN W0200
XX W0200
AX W0200

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mest Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                     21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK34270 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1141 GAAATCTGACACCAGTTTCA 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081 TAACACAAACTTAATAGATTAAAACAGCACGGATTTATTCTCACATGTTTTGAGACGCCA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, pellepsy and cancers. The present sequence is one of the probes of the
                                                                                                                         04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing
                                                                                 30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                      WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK34270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483446/52.
                                                                                                                                                                                     30-JAN-2001;
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  microarray;
                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGTCTGAAATCAGTAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTACCCAAACTTGGTTGTATAAAACAACACACATTTATTCTCTTATAGTTCTGGAGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG
                                                                                                                                                                                                                                                                                                                                                                                                              bone marrow expressed single exon probe
                                                                                                                                                                                                                                                                                                                                                                        bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                                                                                                                                                                                                                                     cancer;
                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-02363359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                       2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DK,
                                                                                                                                                                                                                                                                                                                                                     expressed exon;
; leukaemia; lymp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 110 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43.2; DB Pred. No. 0.011; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
                                                                                                                                                                                                                                                                                                                                                     lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>Ģ</u>
                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                                                                                                                                                                                        expression analysis;
                                                                                                                                                                                                                                                                                                                                                  myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Η;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO: 8827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression
                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                        probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              samples,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419
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RESULT 14
AAI39993/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                   21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                            genetic
                                                                                                                                                                                                                                                                                                                                                                 )993/c
AAI39993 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic ac
                           analyzing
                                                                              Penn
                                                                                                                                                 03-AUG-2000;
                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                            04-FEB-2000;
                                                                                                                                                                                                 30-JAN-2001;
                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                      WO200157272-A2
                                                                                                                                                                                                                                                                                     Probe; microarray;
                                                                                                                                                                                                                                                                                                          Probe #8679 used to measure
                                                                                                                                                                                                                                                                                                                             17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                 AAI39993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1081 TAACACAAACTTAATAGATTAAAACAGCACGGATTTATTCTCACATGTTTTGAGACGCCA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analyzing
                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                   418
                                                                                                                                                                                                                                                                                                                                                                                                                                                         478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                          2001-488897/53.
                                                                              SG,
                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGTCTGAAATCAGTAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAATCTGACACCAGTTTCA 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACCCAAACTTGGTTGATTAAAACAACACACATTTATTCTCTTATAGTTCTGGAGTCCA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
                                      genome-derived single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
57; Conserv
                                                                                                 MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                             disorder;
                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \ensuremath{\mathsf{Dme-derived}} single exon nucleic acid probes gene expression in human bone marrow -
                                                                              Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO: 8827;
                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                 2001WO-US00663
                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 195 A; 110 C; 131
                           expression
                                                                              DK,
                                                                                                                                                                                                                                                                              SS
                                                                                                                                                                                                                                                                                                                                                                  DNA; 585
                                                                                                                                                                                                                                                                                      human;
                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%;
                                                                             Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
       654pp; English
                           in
                                                                                                                                                                                                                                                                                      placenta;
                                                                              ξ
                                                                                                                                                                                                                                                                                                          gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          658pp + Sequence Listing;
                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43.2; DB Pred. No. 0.011; 0; Mismatches
                            human
                                                                             Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                      nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>و</u>;
                           placenta
                                                                                                                                                                                                                                                                                       antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 T;
                              acid
nta –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                     probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                      useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid
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Claim

SEQ

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No

8679;

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RESULT 15
ABS08999/c
ID ABS08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
nucleic acid probes for measuring gene expression in a sample derifrom human lung comprising single exon nucleic acid probes having 12614 nucleic acid sequences mentioned in the specification, or the complements or the 12387 open reading frames derived from the 1261
                                                    The invention relates to a spatially-addressable set
                                                                                                          measure
                                                                                                                      Spatially-addressable
                                                                                                                                                                                                                                                        03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                   26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                           WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081 TAACACAAACTTAATAGATTAAAAACAGCACGGATTTATTCTCACATGTTTTGAGACGCCA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS08999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1141 GAAATCTGACACCAGTTTCA 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478
                                                                                                                                                                            SG
                                                                                                                                                 2002-114183/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGTCTGAAATCAGTAACA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACCCAAACTTGGTTGTTTAAAACACACACATTTATTCTCTTATAGTTCTGGAGTCCA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome-derived single exon probe from lung SEQ ID No 8990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
57; Conserv
                                                                                                                                                                                                   MOLECULAR DYNAMICS
                                                                                                          gene
                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 585
                                                                                                                                                                          Hanzel
                                                                                                                                                                                                                           2000US-180312P.
2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
2000US-236359P.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                Ħ
                                                                                                        expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 195 A; 110 C; 131 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                               No 8990;
                                                                                                                                                                         DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.2%;
                                                                                                                                                                          Chen
                                                                                                                    set of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.9%;
                                                                                                         in
                                                                            634pp;
                                                                                                                                                                         ¥,
                                                                                                         human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43.2;
Pred. No. 0
                                                                                                                                                                          Rank
                                                                               English.
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                                     of single exon
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                                                                                                                                                                                                                                                                                                                                                      CC comprising (a) identifying exons from genomic sequence by the method CC above and (b) measuring the expression of each of the exons in several CC tissues and/or cell types using hybridisation to a single exon CC microarrays having a probe with the exon, where a common pattern of CC microarrays having a probe with the exon, where a common pattern of CC the exons should be assigned to a single gene; a peptide comprising one CC city of 12011 sequences, mentioned in the specification, or encoded by the CC probes/open reading frames (ORF). The probes are used for gene cexpression analysis, and for identifying exons in a gene, particularly CC using human lung derived mRNA and for the study of lung diseases CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary CC (COPD), interstitial nung disease (ILD), familial idiopathic pulmonary CC (Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary CC haemosiderosis, pulmonary histlocytosis, lundonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon
                                                                                              Matches
                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene,
                                               1081 TAACACAAACTTAATAGATTAAAACAGCACGGATTTATTCTCACATGTTTTGAGACGCCA 1140
                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electro format directly from WIPO at
  478
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                            probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to
TTACCCAAACTTGGTTGTTTAAAACAACACACATTTATTCTCTTATAGTTCTGGAGTCCA 419
                                                                                                                          Similarity
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Mouse uromodulin p
Drosophila melanog
Chromosome 13q1-q
Human chemically m
Penaeus vannamei g
Pain regulated cDN
Human PG-3 gene.
Loblolly pine SSR
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RESULT 1
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AAC65084 AAC65098 ABL89328 ABL89342 AAK75374 AAI62937 ABK39927 ABK84757 AAX90001 AAX90015 AAD02813 AAF57186 AAH29391 ABN81165 AAQ27097 AAT33800 AAA52145 AAA59870 AAA61238 AAA51987 AAV27591 AAX01921 ABN81102 AAT32454 ABN81131 ABL88366 AAT88014 AAC73648 AAQ33936 AAS34708 Murine interleukin Murine interleukin Murine Interleukin Murine IL-17R poly Drosophila melanog Rat neuronal inmed Babesia microti BM Babesia microti an Babesia microti an Babesia microti an B. microti BMNI-7 Pabesia MNI-7 Murine interleukin
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Microsatellite seg Human genomic DNA Human chemically p Human cDNA differe Babesia microti an Babesia microti an Tumour suppressor Human immune/haema Shrimp polynucleot Fragile X diagnost Shrimp polynucleot Calpain large subu Grapevine ribosoma Rat apoptosis inhi Human DNA for a no

## ALIGNMENTS

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intron
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therapy; gene expression; pharmaceutical; mouse; ds.
/label= Exon
/con_splice=
8074..8818
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/label= Polycloning site of pBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                               animals
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09-JUL-1999;
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                   TCTCTGTAGGTTAGCTTACATAGGAGACAGGAATAAGTGAAGGAGAGAAGGGAGGACATT
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                                                                                                        CCAGCCAGCACTGAGACTGGAATGCATCAAATCCAGAGACCAGAAAGCACGGTGCTAGCA
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GGACCTTGTAAAAAAGCATAGGGCATCAGTAACTAAAGTTACAAAGATAACAATCAGTGG
                                                                                                                                            AGCAAGATGTTTGCCATCTCCAGAGACTTAGACAGCCCAGGAAAGTTTTGTCCTCCCAGGA
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    New isolated nucleic acid genes from Drosophila and
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                                                                 WPI; 2001-656860/75
P-PSDB; ABB68415.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental pharmaceutical; gene; ss.
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                                                                                                                              Venter
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                                                                                                                              JC,
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2000US-0614150
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                                                                                                                            PWD,
detection reagent for detecting for elucidating cell signalling
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RESULT 3
AAH51803/c
ID AAH51803 standard; DNA; 3001 BP
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30-APR-1999
30-APR-1999
14-JUL-1999
27-JUL-1999
29-JUL-1999
29-JUL-1999
28-OCT-1999;
                                         Cohen D, I
Essioux L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                       sbg1; g34665; sbg2
biallelic marker;
                     WPI; 2000-619082/59
                                                                                                                                                                                                  30-MAR-2000;
                                                                                                                                                                                                                       05-OCT-2000
                                                                                                                                                                                                                                            WO200058510-A2
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                         Chromosome
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                                                                                                                                                                                                                                                                                                                                                                     AAH51803;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                           GENSET
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Similarity 66.7%;
90; Conservative
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                                                    Blumenfeld
                                                                                                                                                                                                                                                                                                                        13q31-q33
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                                                                                               990S-0126903
990S-0131971
990S-0132065
990S-0143928
990S-0145915
990S-0146453
990S-0166453
990S-0162288
                                                                                                                                                                                                                                                                                                  sbg2;
                                                                                                                                                                                                                                                                                      2; g35017; g35018; chromosome 13g31-g33; haplotype; polymorphism; schizophrenia; bipolar disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694 A; 498 C; 419 G;
                                                                                                                                                                                                                                                                                                  g35017; g35018; chromosome
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                                                      Chumakov
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Pred. No. 2.7e-07;
0; Mismatches 45
                                                                                                                                                                                                                                                                                                                       marker containing amplicon
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                                                    Bougueleret L,
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Polynucleotides comprising

sequences

from

sbg1 and

g35018

biallelic

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RESULT 4
ABN80093/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC AAH51601 represents a human genomic nucleotide sequence comprising sbg1, CC 934665, sbg2, g35017 and g35018 nucleic acid sequences located on the CC human chromosome 13g31-g3 locus. The nucleotide sequences contain CC biallelic markers and polymorphisms. Sequences AAH51602 - AAH51625 and CC AAB62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and protein CC products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent g35018 CC CDNA sequences and protein products. Primers AAH51632 - AAH51639 are used to isolate sbg1 cDNAs, while sbg1 exons from different primates are cC represented by sequences AAH51642 - AAH51699. Nucleotide sequences of CC amplicons which comprise biallelid markers located on the chromosome CC 13g31-g33 locus are represented in AAH51819. Nucleotide sequences of CC primers AAH51818 and AAH51819 are used in the isolation of sequences of CC primers AAH51818 and AAH51819 are used in the isolation of sequences of CC used to determine the identity of the nucleotide at a biallelic marker in a sample DNA sequence. The nucleotide sequences may be labelled and used CC a sample DNA sequence. The nucleotide sequences may be labelled and used CC primers Halfelic marker in a biological sample from single or multiple Subjects. By determining the frequency of a biallelic marker in a copulation and association between a genotype and a trait, a haplotype and copulation and phenotype and a trait can be detected. The sequences can be used to determine a predisoposition to or early onset of schizophrenia or bipolar disorder or a beneficial response to or side effects related to creating the internal or bipolar disorder or a beneficial or bipolar disorder.
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Best Local
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                                                                                                                                                                                                                                                        heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation antidiabetic; cytostatic; anticonvulsant; ds.
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01-SEP-2000;
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                                                                                       02-JUL-2001;
                                                                                                                                                                WO200200927-A2
                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            ABN80093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment against schizophrenia or bipolar disorder.
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                                                                                                                                                                                                                                                                                                           development; homeobox gene; HOX; dlabetes; cancer; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                  2000DE-1032529
2000DE-1043826
                                                                                       2001WO-EP07536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 8447
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                                                                                                                                                                                                                                                          SNP; cytosine methylation;
ds.
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(EPIG-) EPIGENOMICS

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least 18 bases in length of a segment of chemically pretreated DNA (II) cof genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADPN, or APD1 and comprising one of 350 CC sequences (ABN79984-ABN80333) or their complements. The invention is CC useful for the diagnosis or therapy of diseases associated with CC development genes, in particular disease related to homeobox containing CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related to disconsist of the brain and limb girdle muscular dystrophy and dwarfism. CC development of the brain and limb girdle muscular dystrophy and dwarfism. CC in amplification of the 350 sequences, as primer oligonucleotides for the amplification of the 350 sequences, as primer oligonucleotides for CC single nucleotides for detecting the cytosine methylation state and/or single nucleotides for this patent did not form part of the printed specification but is based on sequence information supplied to Derwent by XX
                                                                                                                                                                                                                                                                                                             RESULT 5
AAT68682
      밁
                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                           Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 91
                                                                                                                                                                                                                                                                                                                                                                              4002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01ek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                  satellite
                                                                                                                  Penaeus vannamei
                                                                                                                                                aquaculture;
                                                                                                                                                                 Penaeus vannamei; marker;
                                                                                                                                                                                                  Penaeus
                                                                                                                                                                                                                                                                  AAT68682;
                                                                                                                                                                                                                                                                                                AAT68682 standard;
                   repeat_unit
                                                                                                                                                                                                                                  24-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                              ATTAAAACTACTTTAAAAA 3984
                                                                                                                                                                                                                                                                                                                                                                                                                                                              development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą,
                                                                                                                                                                                                                                                                                                                                                                                                          ATATTTCTCACTTTGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACACACACACACACACACACACGCATAACAAATCAAATCCCAAACTAAATACAAAA 4003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-130908/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                 vannamei genomic DNA marker insert from plasmid pPV12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                reproduction;
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    вP;
/note= "Satellite region containing CA repeat units" 246..247
/*tag= b
                                                                  246..408
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1957 A; 144 C;
                                                                                                                                                                                                                                                                                                DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%;
                                                                                                                                                                                                                                                                                              448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27pp;
                                                                                                                                                                                                                                                                                                                                                                                                            1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin
                                                                                                                                                  satellite; microsatellite; shrimp; rep
; growth; size; disease resistance; ds.
                                                                                                                                                growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62.2; DB 24; Pred. No. 9.3e-07; 0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2021 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                 repeat;
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RESULT 6
ABL88369
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                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                      1660
                                                                                                                                                                                                                                                       1600
                                                                                                                                                                                                                                                                                                                                                           farming) of favourable growth features, e.g. increased reproduction, growth rate and size, better disease resistance, growth in cold water and improved aquaculture production. Species, strains and individuals
                                                                                                                                                                                                                                                                                                                                                                                    shrimp's genome. The presence and pattern of the marker are used to characterise the shrimps, specifically for selection (for commercial
                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a specifically claimed genomic sequence of Penaeus vannamei shrimps which can be used as a marker to select Penaeus shrimp having a predetermined genetically transmitted characteristic. The marker comprises a nucleotide repeat present in the
         03-AUG-2000;
                       03-AUG-2001; 2001WO-EP09011
                                       14-FEB-2002
                                                       WO200212338-A2
                                                                       Rattus sp
                                                                                     neurodegenerative
                                                                                               Pain;
                                                                                                              Pain regulated cDNA sequence
                                                                                                                                               ABL88369;
                                                                                                                                                              ABL88369 standard;
                                                                                                                                                                                                                                                                                       1540
                                                                                                                                                                                                                                                                                                                                      Sequence 448
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2;
                                                                                                                              16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-332803/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bagshaw JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WORC-) WORCESTER POLYTECHNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9721835-A2
                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                      also be identified.
                                                                                                                                                                                                                                                                    ATATTT 1665
                                                                                                                                                                                                                                     ACACACACACACGCATGCACACGCACCACACACAAACTGCAAAAGTGAATAAAAAG 1659
                                                                                      analgesic; gene therapy; neurological disorder;
degenerative disease; gene; ss.
                                                                                                                                                                                                       ACTCTT
                                                                                                                                                                                                                                                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ៥
                                                                                                                                                                                                                                                                                                                                                                                                                                                           containing nucleotide repeats for selecting Penaeus shrimps to select for characteristics advantageous in aquaculture
                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 21;
                                                                                                                                                                                                      426
                                                                                                                                                                                                                                                                                                       Conservative
        2000DE-1037759
                                                                                                                                                                                                                                                                                                                                     BP; 169 A; 130 C; 41 G; 108 T; 0 other;
                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buckholt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0570751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US19568
                                                                                                                                                                                                                                                                                                                                                                                                                                            26pp; English.
                                                                                                                                                              cDNA;
                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                             3.1%;
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                                                                                                                                                              3032 BP
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                                                                                                               12
                                                                                                                                                                                                                                                                                                             Score 62; DB 18;
Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                     448;
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RESULT 7
AAF24497/c
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Matches 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises (1) incubating a test substance with a cell (or preparation from it) that has synthesised a peptide or protein (B) and (il) measuring either binding of the test substance to (B) or some functional parameter that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analgesic activity. (A) along with nucleic acid (ABL88411-ABL88441) that encode proteins (B) and agent has BBS5006-ABB85037) that interact with (A); (B); vectors containing the nucleic acid; antibodies against (B); cells that express (B) and agents that bind to (B), are all useful for treating pain, particularly chronic pain, including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The present sequence is that of a polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1480
                                                           primer_bind
                                                                                                   primer_bind
                                                                                                                                                              misc_feature
                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                        AAF24497;
                                                                                                                                                                                                                                                                                                                                                                                                                              AAF24497 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1420 TACAAGAAGAACTTACATGGGACCTTGTAAAAAAGCATAGGGCATCAGTAACTAAAGT 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identifying pain-regulating substances (A) comprises (1) incubating a test substance with a cell (or preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying pain-regulating compounds, useful for treating chronic pain and for diagnosis, by measuring binding of compounds to specific peptides and proteins -
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                23-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3032 BP; 986 A; 615 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Fig 7; 213pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gillen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHEF ) GRUENENTHAL GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACACACACACACACACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACACACACACACGCATGCAC 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAACACCCAGGATTTTCCTGTAACCTTCATATTGATACACATGTACTACTCTGAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-257469/30
                                                                                                                                                                                                                                                                                                      PG-3 gene
                                                                                                                                                                                                                                                                PG-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wetzels I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                              (first entry)
/*tag= b
1980..1998
/*tag= c
1987..2011
/*tag= d
                                                                                               /*tag= a
/note= "5'
1823..1840
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                . 2000
                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA; 240825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%;
                                                                                                                                                                                                                                                                  BRCA1;
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                                                                                                                      regulatory
                                                                                                                                                                                                                                                                  chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      752
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Pred. No. 1e-06;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  586 G; 841 T; 4 other;
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                                                                                                                      region'
                                                                                                                                                                                                                                                                  8p23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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exon primer_bind	exon	GAC I	P X CD	exon	exon	primer_bind	allele	primer_bind	allele	misc_binding	primer_bind	primer_bind	allele	misc_binding	primer_bind	exon	primer_bind	primer_bind	exon	primer_bind	allele	misc_binding	primer_bind	primer_bind	primer_bind		0	CDS	primer_bind	allele
39704.40858 /*tag= ag /label= "T" 39556.39574	3737737466 /*tag= af /label= "S"	/tag= ae /tabel= "F"	/*tag= ad /label= "E" 34261 3404		2681026897 /*tag= ac	1041110430 /*tag- ab	replace(10370,) /*tag= aa	/*tag= z /*tag= z	е,	1027410298 /*tag=_x	1026710285 /*tag= w	complement(1022910247) /*tag= v	<pre>/note= " binds probe" replace(10228,T) /*tag=</pre>	0240 t	/label= "C" 10209.10227 /*tag= s	1011510233 /*tag= r	10007.10025	/label- "B" /1abel- "B" /1451.4908	/*cay= 1: 46274718 /*tag=	æ	Φ.	4589.4613 · /*tag= 1	4582.4600 /*tag= k	4559.4577 /*tag: 4	/ 14001	/+tag= n	/product=""FG-3" /note="this sequence contains introns" 2001 2070	2388 g	me	/note= " binds probe" replace(1999,C) /*tag= e
FT all	<b>.</b>			_	_	_	Δı.	FT mis		,		-	٥.	FT mis	- H-	01		1 75	שי	<b>"</b> C	FT pri	ໝ		ъ	m	ď	ρı		77	FT pri
FT allele /*tag- bn complement(67476	misc_b	primer		FT exon	_		FT FT allele	FT misc_binding	FT primer_bind	primer	primer	-	٥.	-	FT primer_bind	FT allele	FT FT COLUMN	1 75	FT primer_bind	FT primer_bind	יסי	FT allele	FT misc_binding	FT primer_bind	FT primer_bind	FT primer_bind	FT allele	FT misc_binding	FT primer_bind	FT primer_bind FT

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RESULT 8
AAA74226/
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Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                 234624
                                                                                                                                                                                                                                             1525 GTTTTTTTGTTATGAAACACACGCACAGGCACAGGCACTCACGTGTGCGCACGCGCGCA 1584
                                                                                                  Loblolly pine; Simple Sequence Repeat; SSR; genetic marker; mapping; inheritance study; plant breeding programme; ss.
                                                                                                                                                                                                                                                                                                               primer_bind
                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                   primer_bind
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                                                                                       Pinus taeda
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                                                                       WO200042210-A2
                                                                                                                                 Loblolly pine
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                     15-JAN-1999;
19-JAN-1999;
                                           06-JAN-2000; 2000WO-US00325
                                                                                                                                                29-NOV-2000
                                                                                                                                                                                    2
                                                                                                                                                                                                                CACACACACGCGCACACACACACACACGCATGCACACATG
INT PAPER CO
ECHT C S.
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                 /label= "H"
73099..73117
/*tag= cr
                                                                                                                                 SSR locus RIPPT106
                     99US-0232884
99US-0232785
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/*tag= bv

72698..72715

/*tag= bw

72819..72837
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/*tag== h+
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                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
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..69200
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binds
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                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                          No. 1.9e-05;
No. 1.9e-05;
Smatches 26;
                                                                                                          microsatellite DNA population genetics
                                                                                                                                                                                                                              1626
                                                                                                                                                                                                                 234583
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                         240825;
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RESULT 9
AAA74225/c
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                                                                                          (INTO ) INT PAPER CO.
(ECHT/) ECHT C S.
(NELS/) NELSON C D.
(USDA ) US SEC OF AGRI
       Polynucleotide having simple sequence repeat useful as markers plants for genetic characterization e.g. genetic mapping study, inheritance study of a commercially important trait in a plant
                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a loblolly pine Simple Sequence Repeat (SSR) locus. SSRs are also known as microsatellite DNA repeats. The present sequence is useful as a genetic marker for genetic mapping, population genetics studies and inheritance studies in various plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide having simple sequence repeat useful as markers in plants for genetic characterization e.g. genetic mapping study, an inheritance study of a commercially important trait in a plant breeding
                                                                                                                                                                                                                                                                      Loblolly pine; Simple Sequence Repeat; SSR; microsatellite DNA repeat; genetic marker; mapping; inheritance study; population genetics study;
                                                                                                                                                                                                                                                                                                                                                                     AAA74225 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 30; 57pp;
                                                                       Echt CS,
                                                                                                                                             15-JAN-1999;
19-JAN-1999;
                                                                                                                                                                             06-JAN-2000; 2000WO-US00325
                                                                                                                                                                                                 20-JUL-2000.
                                                                                                                                                                                                                     WO200042210-A2
                                                                                                                                                                                                                                          Pinus
                                                                                                                                                                                                                                                             plant
                                                                                                                                                                                                                                                                                                                           29-NOV-2000
                                                                                                                                                                                                                                                                                                                                                AAA74225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-482836/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Echt CS,
                                                                                                                                                                                                                                                                                                       Loblolly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USDA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NELS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       2000-482836/42
                                                                                                                                                                                                                                          taeda
                                                                                                                                                                                                                                                            breeding
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US SEC OF AGRIC.
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                                                                                                                                                                                                                                                                                                       pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelson CD;
                                                                      Nelson CD;
                                                                                           SEC OF AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                        SSR
                                                                                                                                                        9905-0232884
                                                                                                                                                                                                                                                            programme; ss
                                                                                                                                               99US-0232785
                                                                                                                                                                                                                                                                                                        locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 67 C;
                                                                                                                                                                                                                                                                                                                                                                      279
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                                                                                                                                                                                                                                                                                                                                                                     BP.
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Pred. No. 6.3e-07;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 369;
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breeding

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RESULT 10
AAQ55246/c
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Best Local :
                The sequences given in AAQ55231-50 are derived from ribosomes of grapevine genus Vitis. These sequences represent the IGS region the ribosomal (r)DNA repeat and contain polymorphisms. These polymorphisms may be used in a method for the identification of different grape cultivars. These clones contain simple repeat sequences and were identified in a genomic library of grapevine using simple di-, tri- or tetra- nucleotide repeats such as (AT)
                                                                                                                                                                                                                                                                                                                                                                                                      Grapevine ribosomal clone INVGT19C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ55246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1600
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                                                                                                 Claim
                                                                                                                   Novel ribosome DNA probe of grape cultivars
                                                                                                                                                                                                                                                                                                     primer_bind
                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                       Vitis
                                                                                                                                                                                                                                                                                                                                                                         grape
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ55246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 279 BP;
                                                                                                                                                  WPI; 1994-035083/04
                                                                                                                                                                                         (CSIR ) COMMONWEALTH
                                                                                                                                                                                                             03-JUL-1992;
                                                                                                                                                                                                                                 30-JUN-1993;
                                                                                                                                                                                                                                                   20-JAN-1994
                                                                                                                                                                                                                                                                       WO9401580-A
                                                                                                                                                                                                                                                                                                                        primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 ACACACACACACACACACACACACACATATCACAAATTATACACGCAAAAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                       vinifera
                                                                                                                                                                                                                                                                                                                                                                         cultivar;
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          (CGT)10 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                Fig
                                                                                                                                                                                                                                                                                                                                                                                   grapevine;
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                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                                                               93WO-AU00320
                                                                                                                                                                                                                                                                                       /*tag= a
complement
/*tag= b
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76..100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.
         such like
                                                                                                                                                                                                                                                                                                                                                                                  Vitis; IGS region; rDNA; polymorphism;
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                                                                                                                                                                                          SCI & IND
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                                                                                                English.
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                                                                                                                             sequences
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Pred.
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                                                                                                                                                                                          RES
                                                                                                                                                                                                                                                                                                                                                                          detection;
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No. 7e-07;
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                                                                                                                              the
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                                                                                                                              identification
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1644 1811 1584

1869 1525

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RESULT 11
AAX79360/c
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Best Local:
                           Matches 109;
                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the gene encoding the rat apoptosis inhibitory factor PCTF35. The sequence was isolated from rat pheochromocytoma PC12 cells transformed with the human bcl12 gene. The protein can be used for the treatment of apoptosis-caused diseases, including those due to nerve cell death, e.g. Parkinson's disease and Alzheimer's disease.
                                                                                                                                                                 New protein obtained by culturing pheochromocytoma tbcl2 gene as a protooncogene, useful in remedies for apoptosis-caused diseases. e.g. Alzheimer disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                 Sequence
                                                                                                                                                                                                        WPI; 1999-395180/33.
P-PSDB; AAY14570.
                                                                                                                                                                                                                                       Ohsawa
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12-DEC-1997;
                                                                                                                                                                                                                                                                                                         11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                       Nootropic; neuroprotective; apopt pheochromocytoma cell; PC12 cell; Parkinson's disease; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                               Rat
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                                                                                                                                                Example
                                                                                                                                                                                                                                                         (TAIS ) TAISHO
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                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis
TTGTTATTGTTATATTCTATTTTTACTGTTTGTGGCCAGCCTAAGTTGGTCTTGAACTCACT
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                                                                                                                                                                                                                                      ۲,
                                                                                                                                                2
                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                   1645 BP;
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                                                                                                                                                                                                                                      Uchiyama
                                                                                                                                              Page 39-43; 50pp; Japanese.
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitory factor PCTF35
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97JP-0343112.
                                                                                                                                                                                                                                                                                                          98WO-JP05609
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                                                                   359
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                                    3.0%;
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                                                                  A; 472
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                           0,
                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis inhibitory cell; human; bcll2; r
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Pred. No. 9.5e
0; Mismatches
                          Score 59.6; DB 20 Pred. No. 2.1e-06; D; Mismatches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                  459 G;
                                                                                                                                                                                                                                                                                                                                                                                        disease;
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                                                                   355 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                            64;
                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                  nerve
                                                                                                                                                                                                                                                                                                                                                                                                           factor; PCTF35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                           Indels
                                               Length
                                                                                                                                                                                      transformed by
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                                                 1645;
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                                                                                                           be used for
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RESULT 12
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14-AUG-2000
14-AUG-2000
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                          11-JUL-
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07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200155312-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal tissue antigen; ds; antiinflammatory; neuroprotectiv, immunomodulator; cardiovascular; cytostatic; nephrothropic; cardiovascular; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; cancer; hyperproliferative disorder; breast neoplasm; cancer; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral isohaemia, anglogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1870
                                                                                                                                                                                                                                                                                                               07 - JUL-
                                                                                                                                                                                                                                                                                                                                                           07-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-2001
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                                                                                                                                                                                                               14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                          26-JUL-2000,
26-JUL-2000,
                                                                                                                                                                                                                                                                                                                                                 28-JUN-2000
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                                                                                                                                                                                                                                               14 - AUG - 2000
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17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                      9-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for a novel foetal antigen,
2000US-0225213
2000US-0225213
2000US-0225213
2000US-022526
2000US-022526
2000US-022526
2000US-022528
2000US-0225447
2000US-0225757
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2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0215135.
2000US-0216647.
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2000US-0205515.
2000US-0209467.
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2000US-0186350.
2000US-0189874.
2000US-0190076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection;
  02-0CT 2000

02-0CT 2000

02-0CT 2000

02-0CT 2000

02-0CT 2000

13-0CT 2000

13-0CT 2000

20-0CT 2000

20-0CT 2000

20-0CT 2000

20-0CT 2000

20-0CT 2000

20-0CT 2000
08-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                      20-OCT 2000;
20-OCT 2000;
20-OCT 2000;
20-OCT 2000;
01-NOV 2000;
08-NOV 2000;
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                                                                                       08-NOV-2000;
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                                                                                                                                                                   08-NOV-2000
08-NOV-2000
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29-SEP-2000
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27-SEP-2000
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25-SEP-
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2000US-02343703

2000US-0234998

2000US-0234998

2000US-0235836

2000US-02353370

2000US-0235368

2000US-0235368

2000US-02353703

2000US-02356802

2000US-0237037

2000US-0237039

2000US-0241785

2000US-024617

2000US-0246477

2000US-0246475

2000US-0246475

2000US-0246475

2000US-0246611

2000US-0246528

2000US-0246611

2000US-0246525

2000US-0246611

2000US-0246521

2000US-0246521

2000US-0246613

2000US-0249211

2000US-0249211

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2000US-0232397.

2000US-0232399.

2000US-0232399.

2000US-0232400.

2000US-0232401.

2000US-0233063.

2000US-0233064.

2000US-0233065.
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2000US-0239437.
2000US-02319438.
2000US-0231242.
2000US-0231243.
2000US-0231244.
2000US-0231414.
2000US-0231414.
2000US-0231414.
2000US-0232080.
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                                                                                                                                                                                                                                                                                                                                  hyperpoliferative disorders e.g. neephasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, viruses and fungia disorders e.g. corneal infection. The polypeptides can also caused by bacteria, viruses and fungia disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to cregenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. Numerous examples of diseases and disorders treated by the nucleic acids and proteins are given in the specification. The present sequence is a genomic DNA fragment from a gene encoding a foetal antigen of the
                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                   Matches
   10638
                                                                                                                   10578
                                                         1977
                                                                                                                                           be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treatment of the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel nucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g by gene therapy) or ameliorate a meliorate accordation in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the antigens can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       include autoimmune diseases e.g. rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respiratory systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                               Local
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                                 ATATATGTATATATATATACATACA 2001
                                                                                                             ATATATATATATATATATATA 10662
                                                                                                                                                                                                                                   Similarity
69; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID No 2132; 642pp; English.
                                                                                                                                                                                                                          Conservative
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2000US-0249265.
2000US-0249297.
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2000US-0251868.
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2000US-0251988.
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2000US-0249218.
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2000US-0254097.
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2000US-0250391.
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                                                                                                                                                                                                                                                         3.0%;
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                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                            Score 59.4;
Pred. No. 8
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                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                            .le-06;
                                                                                                                                                                                                                                                                                    DB 22;
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RESULT 14
ABL88366
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ABN81131/c
ID ABN811
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                                                                                                                                                                              В
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                             Giant black tiger prawn; Penaeus monodon; pacific whit Litopenaeus vannamei; shrimp; microsatellite sequence; Taura Syndrome Virus; TSV; infection; ds.
Pain regulated cDNA sequence
                                                                                                                                                     1980 TATGTATATATATACATACA 2001
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides of shrimp are useful for identifying, mapping and characterizing of the genome of various species of shrimp
                       16-MAY-2002
                                               ABL88366;
                                                                      ABL88366
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-423422/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alcivar-Warren A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TUFT ) TUFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200034476-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Litopenaeus vannamei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shrimp polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN81131;
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                                                                                                                                193
                                                                                                                                                                              TATATATATATATATATATA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                           67; Conserv
                                                                      standard;
                                                                                                                                                                                                                                                                          849 BP; 121 A; 113 C; 65 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 114; 120pp; English.
                                                                                                                                                                                                                            Conservative
                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLEGE.
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                                                                      CDNA;
                       entry)
                                                                                                                                                                                                                                      3.0%;
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                                                                                                                                                                                                                                       Score
Pred.
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                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                       59.2;
No. 1
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ies 15;
                                                                                                                                                                                                                                                                          T; 398
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                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garcia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shrimp;
                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                      (I), the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mapping;
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                           useful
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RESULT 15
AAT88014/c
ID AAT880:
XX AAT880:
AC AAT880:
XX Z2-APR
XX Z2-APR
XX DE Murine
XX
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Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to identifying pain-regulating substances (A) comprises (1) incubating a test substance with a cell (or preparation from it) that has synthesised a peptide or protein (B) and (ii) measuring either binding of the test substance to (B) or some functional parameter that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analgesic activity. (A) along with nucleic acid (ABL8841-ABL88441) that encode proteins (B, ABB85006-ABB85037) that interact with (A); (B); vectors containing the nucleic acid; antibodies against (B); cells that express (B) and agents that bind to (B), are all useful for treating pain, particularly chronic pain, including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The present sequence is that of a polynucleotide of the invention.
                                                                                                                                                                         1075
                                                                                                                                                                                                                                                                                                                   1480
             Murine IL-5 cDNA genomic fusion
                                                                                                                                                                                                   1600
                                                                                                                                                                                                                               1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; Fig
                                          22-APR-1998
                                                                      AAT88014;
                                                                                                  AAT88014 standard;
                                                                                                                                                                                                                                                                                                                                                                       1420 TACAAGAAGAACTTACATGGGACCTTGTAAAAAAGCATAGGGCATCAGTAACTAAAGT 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying pain-regulating compounds, useful for treating chronic pain and for diagnosis, by measuring binding of compounds to specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000; 2000DE-1037759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2001; 2001WO-EP09011
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1721 BP; 605 A; 342 C; 264 G; 457 T; 53 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-257469/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pain;
                                                                                                                                                                                                                                                                                       955
                                                                                                                                                                                                                                                                                                                                               895
                                                                                                                                                                                                                                                                                      AAAACACCCAGGATTTTCCTGTAACCTTCATATTGATACACATGTACTACTCTGAAGAAA
                                                                                                                                                                       ACACACACACACACACACACAC
                                                                                                                                                                                                                                                                                                                ACACACACACACGCATGCAC 1621
                                                                                                                                                                                                                            analgesic; gene therapy; neurological disorder;
degenerative disease; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRUENENTHAL GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; 213pp; German.
                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%;
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CC This is a murine interleukin-5 (IL-5) cDNA genomic fusion gene. This CC transgenic construct contain a chimeric pIL-5. EXPNNA sequence, comprising CC thymocyte/T cell, lung or basal keratinocyte specific transcription CC control sequence (TCS) and a segment encoding interleukin-5 (IL-5), which CC lacks endogenous 5'-control sequences when the TCS is thymocyte/T cell CC specific. The TCS is usually from a murine CD3delta gene. The chimeric CC DNA sequence is integrated into the genome and causes IL-5 to be CC expressed at a eosinophil related disease inducing level, specifically a CC expressed at a eosinophil related disease inducing level, specifically a CC expressed at a eosinophil related disease inducing level, specifically a CC genumonia, myalgia, Loffler's syndrome, allergy, emphysema, pulmonary CC fibrosis, Wagener's granulomatosis, adult respiratory distress syndrome CC (ARDS), bacterial or fungal infection, leukaemia, rheumatoid arthritis, CC antagonists which are potential therapeutic agents for an IL-5 associated disease to the both levels associated acceptable therapeutic agents for an IL-5 associated disease mbos mice constitution acceptable therapeutic agents for an IL-5 associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic mouse with interleukin-5 gene integrated into its genome - under control of thymocyte and T cell, lung or basal keratinocyte specific regulator, useful as disease model or to screen therapeutic
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therapy; gene expression; pharmaceutical; mouse; ds.
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## ALIGNMENTS

AAK84942 ABV55755 ABV55454 AAL18661 AAL09989 AAL36230 AAX79343

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Human breast cance
Human musculoskele
Human NADH dehydro
Human fibrillin 3

breast

Human Human Human

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Human immune/haema

Human Human

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                                                                                                                   CCGAGGGCTTTACAGGGGATGGTTGGTACTGTGAGTGCTCCCCAGGCTCCTGTGAGCCAG
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ACGCGGGTCTGCACGGCTGGTACCGG
                   ACGCGGGTCTGCACGGCTGGTACCGG
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02-OCT-2000
          Screening for anti-neoplastic agent involves exposing cells chemical agent to be tested for anti-neoplastic activity, ar determining a change in expression of a gene of a signature
                                                                                   Young
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stomach; lung;
cytostatic; gen
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                                                                                                        AVALON
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2000US-237425P
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2000US - 235082P

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2000US - 23537P

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                                                                          GAGTGCTCCCCGGGCTCCTGCGGGCCGGGGTTGGACTGCGTGCCCGAGGGC
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                                                         GTGGATGAGTGCGCTGAGCCTGGGCTTAGCCACTGCCACACGCCCTGGCCACATGTGTCAAT
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73.5%;
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Pred. No. 1.
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Kidney cancer related gene sequence SEQ ID NO:6855

ABL68518 sta ABL68518; 15-MAY-2002

(first entry)

standard;

DNA;

ВP

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05-JUN-2000

18-SEP-2000

118-SEP-2000

20-SEP-2000

20-SEP-2000

22-SEP-2000

25-SEP-2000

25-SEP-2000

25-SEP-2000

25-SEP-2000

25-SEP-2000

25-SEP-2000

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27-SEP-2000

26-SEP-2000

27-SEP-2000

28-SEP-2000

29-SEP-2000

20-OCT-2000

02-OCT-2000

02-OCT-2000

03-OCT-2000

             anti-neoplastic agent to be test
                                                                                        Screening for anti-neoplastic agent involves exposing cells to chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature generation.
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stomach; lung; pr
cytostatic; gene
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present invention describes a method (M1) for screening for an i-neoplastic agent. The method involves exposing cells to a chernit to be tested for anti-neoplastic activity, determining a charsession of at least one gene (I) of a signature gene set, where
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pancreas; carcinoma; antitumour; cancerc
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 Homo sapiens
                                       cytostatic;
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                                      ch; cancer; colon; l
ch; lung; prostate
tatic; gene therap
                                                                                          cancer
                                                                                                                                                                      standard;
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(first entry) related

DNA;

2353

ВP

prostate; ]
ie therapy;

breast; gene

sequence

SEQ IJ

NO:7209.

pancreas; antineoplastic;

ovary; oesophagus; kidney; thyroid; reas; carcinoma; antitumour; cancero

Wilm's

adenocarcinoma;

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comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGAGTATGGTGTGGGCTACTCCTGTGACGCGGGTCTGCACGGCTGGTACCG
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a
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                                                                                                                                       Claim 1;
                                                                                                                                                        Screening for anti-neoplastic agent involves exposing cells to chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature generation.
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02-NOV-2000; 2000WO-US30396

10-MAY-2001

WO200132927-A2

04-NOV-1999;

99US-0163508

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology.
                                                                                                                                                                                  1173
                                                                                                                                                                                                                                                                                                                                1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences (I) (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 275-276; 327pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                         GAGTGCTCCCCAGGCTCCTGTGAGCCAGGACTGGACTGCTTGCCCCAGGGCCCGGATGGA 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAGATGGTGCTCTGAATGTCACAGCAATGCCACCTGCACGGAGGATGAGGCCGTTACG 388
                  ACAGAGTATGGTGTGGGCTACTCCTGTGACGCGGGTTTGCACGGCTGGTACCG 1345
                                                                                                                                                                                                                                         TCGTTTAAGTGCTCCTGTCAGGATGGTTTTTCGTCTGAGGCTGAGCTGAGCTGCACTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCGCCATTCCTGGAGCTCACAACTGCTCCGCCAACAGCAGCTGCGTAAACACGCCAGGC
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                                                                      GAGTGCTCCCCGGGCTCCTGCGGGCCCGGGGTTGGACTGCGTGCCCGAGGGC-----GAC
                                                                                                                                                                                                                      GTGGATGAGTGCGCTGAGCCTGGGCTTAGCCACTGCCACGCCCTGGCCACATGTGTCAAT 628
                                                                                                                                                                                                                                                                                                                              GTGGATGAGTGCTCAGAGCAGGGGCTCAGTAACTGTCATGCCCTGGCCACCTGTGTCAAC 1112
                                                                                                                                                                                                                                                                                                                                                                  TCCTTCTCCTGCGTCTGCCCCGAAGGCTTCCGCCTGTCGCCCGGTCTCGGCTGCACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGCTACCCCATGGACTCACAACTGCT---CCAACAGCAGCTGTGTGAACACCCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGTGCACCTGTCAGGAGGGCTTCACCGGCGATGGCCTGACCTGCGTGGACCTGGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGTGCTCCTGCCAGACCGGCTTCACTGGTGATGGGCTGGTGTGTGAGGACATGGATGAG 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2439 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 A; 707 C; 694 G; 513 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.1%; 73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 283.8; DB 22; Length Pred. No. 1.1e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Ωy 밁 Qy B

ACTGCT---CCAACAGCAGCTGTGTGAACACCCCGGGCTCGTTTAAGTGCTCCTGTCAGG

1014 272 957

213

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TCACT-GCGACGGCCTCGAATGTGCGGATCTGGATGAATGCGCCATTCTGGGGGCGCACACA TCACTGGTGATGGGCTGGTGTGTGAGGACATGGATGAGTGTGCTACCCCCATGGACTCACA CGCCAATGCCACTTGTACGGTGGACGGGGCTTGCCACGACCTGCGCCTGCCAGGAGGGCT

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RESULT 6
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AX 25-P
XX 13-P
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                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                             uromodulin promoter expresses the heterologous gene in vivo in the kidneys to produce a recombinant biologically active protein in the urine. The recombinant proteins produced may be useful for treating human diseases. The major advantages of using this urine-based systems are the ability to harvest the product soon after birth and throughout the life of the animal irrespective of sex or reproductive status, and the ease of product purification from urine. In addition, livestock urine is a proven, currently utilized source of pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New methods to produce heterologous recombinant proteins in require the use of a DNA molecule which is a kidney-specifi promoter, such as the uromodulin promoter, operably linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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09-JUL-1999;
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therapy; gene expression; pharmaceutical; goat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goat uromodulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New kidney-specific promoter useful for production animals as urinary bioreactors, is operably linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1999;
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                                                                                                                                                                                                                                                                                                              Sequence 655 BP; 116 A; 187 C; 211 G; 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heterologous gene encoding a biologically active protein.
                                                                                  94
                                                                                                             CCAGCTGCAGGGATTCTGAAGCTGGGCTCTTCTGTCCGCAGGACGGTGTTCTGAATGCCA 838
CAACCACGCCACCTGCACGGTGGATGGTG-TGGTCACAACGTGCTGCCTGCCAGACCGGCT
                                                                                  CAAGCGGTCCCCACTCTGAATCTGGGCTTTTCTGCCTGCAGAAAGCTGCTCTGAATGTCA
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                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                   Conservative
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99US-0142925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                   0;
                                                                                                                                                                                                                           Score 254.2; DB 2
Pred. No. 9.3e-69;
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                                                                                                                                                                                                   Mismatches 158;
                                                                                                                                                                                                                                                                                                                 T; 3 other;
                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                      Length
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to a heterologous
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       The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic frames are a thereau and chromosom marker procedures.
                                                                                                                                                                                          Claim
                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo diagnostic, forensic, gene therapy and chromosome mapping procedu
    in diagnostic,
                                                                                                                                                                                                                                                                                                                                   (GEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGTGATGTCAGTCTGGGCGGCTGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAATACATATGAGACCCTGACTGACTACTGGCGCACAGAGTATGGTGTGGGCTACT
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    forensic,
                                                                                                                                                                                                                                                                                                                                                              99US-0122487
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                                                                                                                                                                                    8222; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                      Duclert A,
 gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
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                                                                                                                                                                                                                                                                                                      P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tenella;
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Pred. No. 1
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1.4e-18;
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                                                                                                                                                                                                                                       coccidia,
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                                                                                                                                                                                                                                                                                                                                                         Strausberg
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cDNA encoding the GX5401 antigen to identify clones encoding settensions of the GX5401 coding sequence. Several plaques reactive with the cDNA were identified. DNA from clone number 533 was sequenced. This analysis showed that the coding sequence in this clone overlaps with the GX5401 coding sequence and extends that sequence toward the N-terminal coding region. Analysis of the new sequence together with the GX5401 antigen coding sequence reveals an open reading frame encoding an Eimeria

Claim 10; Page 93 and Fig 14; 134pp;

An E.

tenella

genomic library was screened with radioactively labeled

English.

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RESULT 9
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Best Local
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                           16-DEC-1997;
18-DEC-1996;
13-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein of about 250,000 daltons. The protein carries several repeated peptide sequences and is rich in cysteine residues. The open reading frame encodes a potential signal sequence for protein secretion. The coding sequence for this antigenic protein is given in AAN93324. Also new are an expression vector conty. the cloned gene, host cells transformed with the vector, and AP encoded by the cloned gene. The transformed cells are used in a vaccine to immunise birds against avian coccidiosis. By labelling the peptides, they can be used as a type-specific probe. The AP may also be used in an assay to detect Ab against the coccidia. The Abs are used to identify transformed cells conty.
                                                                                                                                                                                                                                                                                                                       Secreted protein; human fetal brain; nutrition; cytokine; stimulant; cell proliferation; differentiation; immune system; suppressor; ligand; regulator; hematopolesis; tissue growth; activin; inhibin; haemostatic; chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1413 CATCGATGAGTGCTCAGAG
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                                                                                                                                                                                                                                                                                                            anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV44292 standard;
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(GEMY ) GENETICS INST INC
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                                                                                                                                                                                                                                                                             sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                    secreted protein clone CB107_1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6567 BP; 1490 A; 1741 C; 2189 G; 1147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                         97US-0991872.
96US-0769192.
97US-0783401.
                                                                                        97WO-US23330
                                                                                                                                                                               /*tag= a
/product= secreted protein
/note= "isolated from clone CB107_1"
                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                            gp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63.8; DB 11
Pred. No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 10
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Best Local
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Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                               1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes a novel secreted protein from clone CB107_1 isolated from a human fetal brain cDNA library. This protein has applications for nutritional use, cytokine and cell proliferation/differentiation activity, immune stimulating or
                                                                                                                            Human; secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
                                                                                                                                                                                                                                                                                                                                                           1158
                                                                                                                                                                                 Human cDNA clone CB107_1 internal sequence
                                                                                                                                                                                                             07-JUN-2001
                                                                                                                                                                                                                                                                AAF98466 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim la; Page 64-65; 110pp; English.
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                                                              WO200119988-A1
                                                                                       Homo sapiens
                                                                                                                 haematopoiesis.
                                                                                                                                                                                                                                       AAF98466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAGCTGCACTGATGTGGATGAGTGCTCAGAGCAGGGGGCTCAGTAACTGTCATGCCCTG
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DB; AAW64219.
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                                                                                                                                                                                                                                                                                                                                                                                    GCTTTATGCTTCAACACTGTTGGAGGACACAACTGTGTTTGCAAGCCGGGCTATACAGGG
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, Spaulding
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                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 205 A; 130 C;
                                                                                                                                                                                                                                                                 CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             libraries
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Treacy M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 T; 4 other;
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14-SEP-2000; 2000WO-US25135

22-MAR-2001

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RESULT 11
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Best Local Similarity
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Human; foetal brain cDNA library; GDP dissociation stimulating protein; brain specific nucleosome assembly protein; diagnosis; therapy; skeletal muscle specific ubiquitin conjugating enzyme; TMP-2; NPIK; nel-related protein type 1; nel-related type 2; hereditary disease;
                                                                                                                        20-APR-1998
                                                                                                                                                                                     AAV01882 standard; cDNA; 2448
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                                                                                                                                                          AAV01882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides and nucleic acids may be used as nutrients or to modulate cytokine and cell proliferation/differentiation activity and may also to involved in modulation of the immune system. The CDNA sequences, proteins, their agonists and/or antagonists exhibit haematopoiesis regulating activity; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 761 BP; 205 A; 130 C; 200 G; 222 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity; receptor/ligand activity; anti-inflammatory activity; haematopoiesis activity; cadherin/tumour suppressor activity; and tumour inhibition activity. Included in the invention are probes represented in AAF98490 - AAF98572 which are specific for the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins AAB90667 - AAB90750. The cDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The
                                                                                                                                                                                                                                                                          494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids encoding polypeptides, useful for modulating e.g. cytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacobs K,
Merberg D,
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                                                                                                                                                                                                                                                                                                                                GCTTTATGCTTCAACACTGTTGGAGGACACAACTGTGTTTGCAAGCCGGGCTATACAGGG
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                                                                                        nel-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the secreted proteins.
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Treacy M
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                                                                                   protein type 2 gene.
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Bowman M
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Pred. No. 1.1e-07;
0; Mismatches 107
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Spaulding V, Agos
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RESULT 12
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Best Local
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            Human nel-related protein type 2 gene.
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                                                                                                                   AAV01883;
                                                                                                                                                              AAV01883 standard;
                                                                                                                                                                                                                                                                                           1549 AATGG 1553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a nel-related protein type 2 isolated a human foetal brain cDNA library. The nucleotide or amino acid sequences are useful for in-vitro diagnosis of hereditary diseases cancer and for preparation of pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human genes, e.g. useful for diagnosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-459830/43.
P-PSDB; AAW37501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAR-1997;
19-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                              GATGG 1162
                                                                                                                                                                                                                                                                                                                                                                                  GCTTTATGCTTCAACACTGTTGGAGGACACAACTGTGTTTTGCAAGCCGGGCTATACAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                 GCCACCTGTGTCAACACAGAAGGCGACTACTTGTGCGTGTGTCCCGAGGGGTTTACAGGG 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCAACACCCCGGGTTCTTTTATGTGCATCTGCAAAACTGGATACATCAGAATTGATGAT 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGAACACCCCGGGCTCGTTTAAGTGCTCCTGTCAGGATGGTTTTCGTCTGACGCCTGAG 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGAAGACATCGATGAGTGTGCTGAAGGGCGCCATTACTGTCGTGAAAATACAATGTGT 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGAGGACATGGATGAGTGTGCTACCCCATGGACTCACAACTGCTCCAACAGCAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGCTGCACTGATGTGGATGAGTGCTCAGAGCAGGGGGCTCAGTAACTGTCATGCCCTG 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2448 BP; 660 A; 521 C; 611 G; 656 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 107-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96JP-0063410
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1..2448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "no stop codon given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "nel-related protein
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                                                                                                                                                                 BP
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Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 107;
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RESULT 13
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AC ABK64
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a nel-related protein type 2 isolated a human foetal brain CDNA library. The nucleotide or amino acid sequences are useful for in-vitro diagnosis of hereditary diseases cancer and for preparation of pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiwara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; Page 109-114; 123pp; English
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                                                                                                                                                                                                 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-459830/43.
P-PSDB; AAW37501.
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19-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; ss.
 18-JUN-2002
                          ABK64420;
                                                    ABK64420 standard;
                                                                                                                     1645 AATGG 1649
                                                                                                                                                                                                                                                                                                                                   1408 TGTGAAGACATCGATGAGTGTGCTGAAGGGCGCCATTACTGTCGTGAAAATACAATGTGT
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                                                                                                                                                                                                                                                                                                                                                             918 TGTGAGGACATGGATGAGTGTGCTACCCCATGGACTCACAACTGCTCCAACAGCAGCTGT
                                                                                                                                              GATGG 1162
                                                                                                                                                                        GCTTTATGCTTCAACACTGTTGGAGGACACAACTGTGTTTGCAAGCCGGGCTATACAGGG
                                                                                                                                                                                       GCCACCTGTGTCAACACAGAAGGCGACTACTTGTGCGTGTGTCCCGAGGGCTTTACAGGG
                                                                                                                                                                                                                            TATTCATGTACAGAACATGATGAGTGTATCACAAATCAGCAC - - - AACTGTGATGAAAAT
                                                                                                                                                                                                                                                    CTGAGCTGCACTGATGTGGATGAGTGCTCAGAGCAGGGGCTCAGTAACTGTCATGCCCTG
                                                                                                                                                                                                                                                                              GTGAACACCCCGGGCTCGTTTAAGTGCTCCTGTCAGGATGGTTTTCGTCTGACGCCTGAG 1037
                                                                                                                                                                                                                                                                                                                                                                                       135;
                                                                                                                                                                                                                                                                                                                                                                                                                                         3198 BP; 900 A; 657 C; 757 G; 884 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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 (first entry)
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96JP-0063410.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                  4.3%;
                                                    DNA; 3198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain-specific nucleosome assembly protein therapy of hereditary disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                      Score 57.8; DB 18;
Pred. No. 6.1e-07;
0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein type
                                                                                                                                                                                                                                                                                                                                                                                                              Length 3198;
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Q В δÃ р

1098

1528 TATTCATGTACAGAACATGATGAGTGTATCACAAATCAGCAC---AACTGTGATGAAAAT

CTGAGCTGCACTGATGTGGATGAGTGCTCAGAGCAGGGGCTCAGTAACTGTCATGCCCTG GTCAACACCCCGGGTTCTTTTATGTGCATCTGCAAAACTGGATACATCAGAATTGATGAT

GCCACCTGTGTCAACACAGAAGGCGACTACTTGTGCGGTGTGTCCCGAGGGCCTTTACAGGG

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QΥ
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                                                                                                                                                                                                                              The invention relates to a method of diagnosing (I) the onset or CC progression of benign prostatic hyperplasia (BPH), or screening (II) for CC or identifying an agent that modulates the onset or progression of BPH. CC The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate CC hyperplasia as compared to normal prostate tissue. (I) comprises CC detecting the expression levels of one or more genes in prostate cells from the subject that are differentially regulated compared to normal CC prostate cells. (II) comprises preparing a first gene expression profile CC agent, preparing a second gene expression profile CC agent, preparing a second gene expression profile of the agent exposed CC (I) is useful for diagnosing the onset or progression of BPH. (II) is CC (I) is useful for diagnosing the onset or progression of BPH. (II) is compression level in a tissue or cells, by comparing the expression CC level of genes given in the specification in the tissue or cells to the CC expression level in a tissue or cells, by comparing the expression CC level of expression of gene in the database, and displaying the CC expression levels of at least one gene in the tissue or cell sample CC expression prostate cancer. ABK64106-ABK64860 represent human CC benign prostatic hyperplasia gene sequences of the invention.
                                                                                                                                            Query Match
Best Local :
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
                                                1408 TGTGAAGACATCGATGAGTGTGCTGAAGGGCGCCATTACTGTCGTGAAAATACAATGTGT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2000; 2000US-223323P
05-JUN-2001; 2001US-0873319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 189-190; 444pp; English
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                                                                                                                                                                                                 Sequence
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                                                                                       918
                                                                                                                           Local Similarity 55...
les 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
GTGAACACCCGGGCTCGTTTAAGTGCTCCTGTCAGGATGGTTTTCGTCTGACGCCTGAG 1037
                                                                    TGTGAGGACATGGÀTGAGTGTGCTACCCCATGGACTCACAACTGCTCCAACAGCAGCTGT 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       benign prostatic hyperplasia gene #315
                                                                                                                                                                                                     3198
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                                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostatic hyperplasia; BPH; prostate cancer; gene;
                                                                                                                                                                                                   900 A; 657 C;
                                                                                                                                            4.3%;
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                                                                                                                             0,
                                                                                                                           Score 57.8; DB 24; Pred. No. 6.1e-07; 0; Mismatches 107;
                                                                                                                                                                                                     757 G; 884 T; 0 other;
                                                                                                                               Indels
                                                                                                                                                                  Length
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03-OCT-2000;
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27-SEP-2000
28-SEP-2000
29-SEP-2000
29-SEP-2000
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27-SEP-2000;
27-SEP-2000;
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02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                       stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.
                                                                                                                                                                                    26-SEP-2000;
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22-SEP-2000;
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18-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer related gene sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1585
                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                  ABL64882;
                                                                                                                                                                                                                                                                                                                                                                                                                              ABL64882 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTTATGCTTCAACACTGTTGGAGGACACAACTGTGTTTGCAAGCCGGGCTATACAGGG 1644
                                                                                                                                                                                                                                                                                                                                                                     cancer;
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                                                                                2000US - 236033P

2000US - 236034P

2000US - 236109P

2000US - 236111P

2000US - 236842P

2000US - 237173P

2000US - 237173P
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2000US-235720P.
2000US-235840P.
                                                                    2000US-237278P.
2000US-237294P.
                                                                                                                                                  2000US-235863P
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                                                                                                                                                                             2000US-235638P
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                                                                                                                                                                                                                                              234034P.
234052P.
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Best Local Similarity
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           cytosine methylation; ds
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                                                                                                                                         1585
                                      Tumour
                                                  18-DEC-2001
                                                                           AAS46333 standard; DNA; 7667
                                                                AAS46333;
                                                                                                             1645 AATGG 1649
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Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVAL-) AVALON PHARM.
                                                                                                                          GATGG 1162
                                    suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Augustus M, Weaver Z;
                                                                                                                                                                                                                                               Conservative
                                                  (first entry)
                                                                                                                                                                                                                                                      4.3%;
55.1%;
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The present invention describes a method (M1) for screening for an C anti-neoplastic agent. The method involves exposing cells to a chemical eagent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in AbL61664 CC to AbL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC activity and can be used in gene therapy. M1 can be used for screening CC an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC treatment of cancer such as colon, breast, stomach, lung, thyroid, CC easophageal, ovarian, kidney, prostate or pancreatic cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, carcinoma, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
Human; tumour suppressor gene; oncogene; antitumour; cancer; tumour; CpG dinucleotide; single-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3198 BP; 900 A; 657 C; 757 G; 884 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          918 TGTGAGGACATGGATGAGTGTGCTACCCCATGGACTCACAACTGCTCCCAACAGCAGCTGT 977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTTTATGCTTCAACACTGTTGGAGGACACAACTGTGTTTGCAAGCCGGGCTATACAGGG
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                                                                                         gene derived chemically modified sequence
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                                                                                                                                                                                                                                                                                                   ВP
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Pred. No. 6.1e-07
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                                    antitumour;
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polymorphism;
                                    cytostatic;
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   SNP;
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Best Local Similarity
Matches 95; Conserv
                                                                                        4617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2000; 2000DE-1013847.
06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
        4677
                                                                                                                                                                                                                                                                                                                                    Sequence 7667 BP; 2446 A; 63 C; 1493 G; 3665 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                            oncogenes.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-602752/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2001; 2001WO-EP02955
                                                                                                                               136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 genomic sequences derived from tumour suppressor genes
                                                                                                                                                                                          76 TAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAGAGAAATGTTCCCTTTGC 135
                                                                                                              AGAAGCAATCTTAATCCCTCTTTTAGCACACCTTGATGTGATCTTTATTTTAAGCCCATTT 195
GTAGTTTTATAATTGTTATTATTTTGATTAGTATTTT
                                            CTCAGATTGTAATGAGCACAGGACTCACTTCGAAGTTT 233
                                                                                      EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID No 55; 27pp; English.
                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.6e-06;
0; Mismatches 63
                                                                                                                                                                                                                                                                                         DB 22;
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Search completed: February 17, 2003, 09:18:44 Job time: 286.868 secs